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&lt;211&gt; 957

&lt;212&gt; DNA

<213> *Staphylococcus epidermidis*

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- 12 -

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&lt;212&gt; DNA

<213> *Staphylococcus epidermidis*

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- 14 -

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- 15 -

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&lt;211&gt; 1881

&lt;212&gt; DNA

&lt;213&gt; Staphylococcus epidermidis

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 <212> DNA  
 <213> *Staphylococcus epidermidis*

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 gatattcaaa atattattaa caatccaaac gatcaagaaa aagagaaaga atttaacaaa 540  
 acagataaaa aagatcattc aacgaacat tgtgactttt tacatcaatc ctcaactaaa 600  
 aacgaacact caccattatc aaatgaacgt gtcgtaccag ttaaaggat tagaaaagct 660  
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aatatctcta ttgctgttgc agacgatgat aagttgtatg tgccagtcac taaaaatgca 960  
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<210> 19  
 <211> 885  
 <212> DNA  
 <213> Staphylococcus epidermidis

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 aagatttcac atatcgattt tattgataga caaattatcc aagagtgtct tggacacctt 180  
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 cccaaatatg aaaagaaatt accagatgtg cttgaaatag acgaagtaat agcattactg 360  
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 aaatcacaaa ttagaaaaat gtatacgcat tttcatccaa gagct 885

<210> 20  
 <211> 2400  
 <212> DNA  
 <213> Staphylococcus epidermidis

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acatctacat attttattat gaaaatacca gatgtgattc gaaataagtt tattgctgtt	180
cgattaccat ggatgccttc aattgatatt aatttagatt taagattaga tggtttaagt	240
ttaatgttcg gcttaattat ttcgctaata ggtgtgggtg tttttttta tgcacgcaa	300
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ttaggcgcca ttcaatcttt catgattaca gtgtttgggt ggctagcgtt attaacagga	540
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aatgcaattt cacgacatcc tttatttata ccaatgattt tgatgctatt attaggtgct	660
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<210> 21  
 <211> 2676  
 <212> DNA  
 <213> Staphylococcus epidermidis

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 aatgatgtaa tcaataatag tcagtcaata aacaccgatg atgataacca aataaaaaaa 180  
 gaagaaacga atagcaacga tgccatagaa aatcgctcta aagatataac acagtcaaca 240  
 acaaatgtag atgaaaacga agcaacattt ttacaaaaga cccctcaaga taatactcag 300  
 cttaaagaag aagtggtaaa agaaccctca tcagtcgaat cctcaaattc atcaatggat 360  
 actgccaac aaccatctca tacaacaata aatagtgaag catctattca aacaagtgat 420  
 aatgaagaaa attcccgcgt atcagatttt gctaactcta aaataataga gagtaacact 480  
 gaatccaata aagaagagaa tactatagag caacctaaac aagtaagaga agattcaata 540  
 acaagtcaac cgtctagcta taaaaatata gatgaaaaaa tttcaaatac agatgagtta 600  
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 attattaaag cacatgatgc tgaaaactta atctatgatg taacttttga agtagatgat 840  
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 aataataaca ctaagttaga tgtagaatat aagacggccc tttcatcagt aaataaaaca 1140  
 attacggttg aatatcaaaa acctaacgaa aatcggactg ctaaccttca aagtatgttc 1200

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acaaacatag atacgaaaaa ccatacagtt gagcaaacga tttatattaa ccctcttcgt 1260
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agtaacagaa tttatgatta cagtgaatat gaagatgtca caaatgatga ttatgcccaa 1440
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aaagttatta gtaaatatga ccctaataag gacgattaca cgacgataca gcaaactgtg 1560
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gatcatgatt ctaaaggcac attacttgga gctttatttg cagggttagg agcgttatta 2640
ttagggaagc gtcgcaaaaa tagaaaaaat aaaaat 2676

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&lt;210&gt; 22

&lt;211&gt; 1452

&lt;212&gt; DNA

&lt;213&gt; Staphylococcus epidermidis

&lt;400&gt; 22

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atgagtgaac gtatcagagt aagatatgcg ccaagtccaa caggatattt gcatattggg 60
aatgcaagaa cagcattatt caattattta tttgctaaac attataatgg tgattttggt 120
gttcgcatcg aagatacaga tagtaaactg aatttagaag atgggtgaatc ttcacaattc 180

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gataatctaa aatgggttagg tttggattgg gatgaatctg tcgataaaga taaagggtttt 240  
 ggaccttata gtcaatctga acgtgcagaa atctataatc cactaattca acagctatta 300  
 gaggaagaca aagcatataa atgttatatg actgaagaag agttagaagc agagcgtgaa 360  
 gctcaaattg ctctgtggaga gatgccaaaga tatgggtggac aacatgcgca cttaacagaa 420  
 gaacagcgtc aacagtacga agcgggaagg cgtaaaccat caattcgttt ccgtgtgcct 480  
 aaagatcaaa catatacttt caatgacatg gttaaaggag aaatttctt tgaatctgac 540  
 aatatcggag actgggtaat tgtaaaaaaa gatggtgttc cgacttataa ttttgcagtt 600  
 gccgtagatg atcattatat gcaaatatca gatgtttatac gtggtgatga ccatgtttca 660  
 aatacaccta agcagttaat gatatatgaa gcatttggat gggaagcacc tcgttttgggt 720  
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 ggtcctgaat tacctaacac aattgaagta ttaggcaaag ataaagtatt gtcacgctta 1440  
 aaaaaccttg tt 1452

&lt;210&gt; 23

&lt;211&gt; 888

&lt;212&gt; DNA

<213> *Staphylococcus epidermidis*

&lt;400&gt; 23

atggaatata aagatatagc aacaccatct cgaacacgtg ctttgcttga tcaatatggg 60  
 ttttaatttta agaaaagttt aggacaaaat tttctaatag atgtaaatat cattaataaa 120  
 attatcgaag cgagtcatat agattgtaca acgggtgtaa ttgaagttgg accaggtatg 180  
 ggatcattga ctgaacaact tgcaaagaat gctaagaagg tgatggcttt tgaaattgat 240  
 caaagattaa tacctgtgct taaagataca ctttcacat acgataatgt aacaattatc 300

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aatgaagata tacttaaagc tgatattgct aaagctgtag atacacatct acaagattgt      360
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ttgatgcaac aggatgtacc tattgatggt tttgtcgtaa tgatgcaaaa agaggtagga      480
gaacgtttga acgctcaagt aggtaccaaa gcatacgggt cgttatcgat tgttgctcaa      540
tactatacgg agacaagtaa agttttaaca gttcctaaaa ctgtatttat gcctcctcca      600
aacgttgatt ctatcgttgt aaaattgatg caacgccaaag aaccacttgt acaggttgat      660
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aataataact accaaaactt ctttaaagat ggtaagaaga ataaagaaac tatacgacag      780
tggctagaaa gcgctggtat tgatcctaaa agacgtggag aaacactcac gattcaagat      840
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<210> 24
<211> 318
<212> DNA
<213> Staphylococcus epidermidis

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<400> 24
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tgtagtctgc aactcgacta tatgaagctg gaatcgctag taatcgtaga tcagcatgct      180
acgggtgaata cgttccccggg tcttgtagac accgcccgtc acaccacgag agtttgtaac      240
accogaagcc ggtggagtaa ccatttggag ctagccgtcg aaggtgggac aaatgattgg      300
ggtgaagtcg taacaagg                    318

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<210> 25
<211> 1326
<212> DNA
<213> Staphylococcus epidermidis

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<400> 25
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gttgctgatg aagaaggttt aaccattact catgcagctg aaacacatat acatgcagat      180
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gaaagtgatg acacgttagg ttataaaaa atgcctaacc agactcattt tgttcaacat      300
aatgatgata tttatgtagg aaatataaaa ttaaaagtgc ttcatacacc tggtcacacg      360
ccagaaagta taagtttttt acttactgat gaaggtgctg gagcacaagt tccaatggga      420
ctattcagtg gtgattttat ttttgtagga gatatcggtg gacctgattt actagaaaaa      480

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 gcaccaccac atcattttgc acaaatgaaa aaaattaatc aattcgggtat gaatttatat 780  
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 tctcaagcgg ttcatgtacc acacggcaaa cttttagaaa cagatttacc tttcaataga 1200  
 aacgatgtta tttatgtaca ctgtcagtct ggcattagaa gttcgatagc tattgggtatt 1260  
 ttagaacata aaggttatca caacattatt aatgtaa atg aaggttacaa agatatacac 1320  
 ctttct 1326

&lt;210&gt; 26

&lt;211&gt; 855

&lt;212&gt; DNA

<213> *Staphylococcus epidermidis*

&lt;400&gt; 26

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 ggtgataaga ctgatactaa agataagaaa gaagaaacaa agcaaacttc aaaggcaaat 120  
 aaagagaaca aagaacaaca tcataagcaa gagaatgata ataaggcttc aactcaattg 180  
 tcagaaaaag aaagggttagc attagcattt tatgcggatg gagtagaaaa atatatgtta 240  
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 aaaaataaaa tatttatagg tagtacgcaa ggcgcactga ttgattatca aacattatta 480  
 aataatggca aggagttaga tattagtcaa ttgtatgaag ataataaaga caatcgctca 540  
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 ataagtgact ttgatggtta gttagataat aaaacttatt tatgggacaa tattagaatc 720  
 aatgacgatg gtaattggac agttcattac cgtaatcatg atggtgaaat tatgggtact 780

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tataagagtg agaaaaataa aattattaaa cttgatcaaa atggaaataa aattaaagaa 840  
 caacaaatgt ctaat 855

<210> 27  
 <211> 1494  
 <212> DNA  
 <213> *Staphylococcus epidermidis*

<400> 27  
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 gatcgtccag gtattgaaag ttctaacgaa agaaacaatg ccggtacagg acatgcggcg 180  
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 atgacaggtc gtactggtaa cgaaatcatg gcggctagta aaatcgacga aggtacagat 540  
 gttaactacg gtgaattaac tcgtaaaatg gcaaaaagta ttgaaaaaca tccaaatgct 600  
 gatgttcaat acaaccacga agtaattaat ttcaatcgtc gtaaagacgg tatttgggaa 660  
 gttaaagtta aaaaccgtaa ttctggagac gttgaaactg ttctagctga ttatgtattt 720  
 atcgggtgcag gcgggtggcg tattccacta ttacaaaaaa ctggtatccc agaaagtaaa 780  
 catcttggtg gattccctat cagtggtcag ttcttaattt gtacaaaccc tgatgtaatt 840  
 aatgaacatg acgtcaaagt atatggtaaa gaaccaccag gcacacctcc aatgactgta 900  
 ccacatttag atacacgtta tatcgatggt gaaagaacat tattatttgg accatttgca 960  
 aatattggcc ctaaattctt aagaaacggt tctaacttag acttattcaa atcagttaaa 1020  
 ccttataaca tcacaacatt actagcatct gcagttaaaa acttaccttt aatcaaatac 1080  
 tctatcgacc aagtattaat gactaaagaa ggttgatga accatctacg caogttctac 1140  
 cctgaagctc gtgacgaaga ttggcaatta tacactgcag gtaaacgtgt tcaagttatc 1200  
 aaagatacta aagaacacgg taaaggattc attcaatttg gtacagaagt tgttaactct 1260  
 aaagaccact ctgttatcgc actattgggt gaatcacctg gagcatcaac ttcagtatca 1320  
 gtagccctag aagttttaga gaaaaacttt gctgagtatg aaaaagattg gactccaaaa 1380  
 ttacaaaaaa tgatcccatc atatggtaaa tctcttatcg atgatgttaa gttaatgaga 1440  
 gcaactcgta aacaaacatc taaagattta gaattaaatt attacgaatc taaa 1494

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<210> 28  
 <211> 1548  
 <212> DNA  
 <213> *Staphylococcus epidermidis*

<400> 28  
 atgaaaatat ttaaaacttt aagttctata ctagttacat ctgttctttc tgtgactgtg 60  
 attccctcaa catttgcac aacagaatct actgctacaa atcagacaca acaaacagta 120  
 ctttttgata attctcatgc tcaaactgcg ggcgctgccg attgggtgat tgatggcgct 180  
 ttctcagatt atgcagattc aatgagaaag caaggttacc aagttaaaga actagaagga 240  
 gaatcaaaca ttctgatca atctttacag caggcgcatg tattagttat tcccgaagct 300  
 aacaatccat ttaaagaaaa tgagcagaaa gcaatcatta attttgtaa aaatgggtgg 360  
 agcgtcattt tcatctcaga ccattataat gccgatcgta atttaaactg tattgattct 420  
 tcagaatcaa tgaatgggta tcgacgtggc gcatacgaaa atatgactaa agatatgaat 480  
 aatgaagaaa agaattctaa cgttatgcat aacgttaaga gttctgattg gctctcacia 540  
 aacttcgggtg ttcgcttttag atataatgca cttggagata tcaatactca aaatatcggt 600  
 tcaagcaaag atagttttgg tattactaaa ggtgtacaat cagtttcgat gcacgcaggt 660  
 tcaacattag caataactga tcctaataaa gctaaaggca ttatttatat gccggaacat 720  
 ttaacgcata gtcaaaaatg gcctcacgca gttgatcaag gtatttacaa tgggggtggc 780  
 atcaacgaag gaccttatgt agccatttca aaaatcggca aaggtaaagc tgcatttatt 840  
 ggcgatagct ccctcgtaga agatcggtca cctaaatatc ttcgtgaaga taatgggaaa 900  
 cctaaaaaaaa cgtacgatgg ttttaaagaa caagataatg gaaagttatt aaataattta 960  
 acaacatggc taggcaaaaa agaattctaa tcttctatga aagacatggg gattaaactt 1020  
 gataataaaa caccgctact taactttgag caacctgaga attcaattga acctcaaaaa 1080  
 gaaccgtgga ctaacccaat agaagggtac aaatgggtatg atcggtcaac atttaaaaca 1140  
 ggtagttatg gaagtaatca acgggggtgct gacgatggag tagatgacaa aagctcttct 1200  
 catcaaaatc aaaatgccaa agttgaatta actttacctc aaaatatcca accgcatcat 1260  
 ccatttcaat ttacaatcaa actcacggga tatgagccta atagcacaat tagcgatgta 1320  
 agagttggac ttataaaga tggaggtaag caaatcggtg gcttttcttc taaccgtaac 1380  
 caattcaata ctctcggtca tagtcctggc caatcaatta aagcaaattg tgcggtgaa 1440  
 gcttcattca cactcacagc taaagtgaca gatgaaatta aagatgctaa tattcgtgtt 1500  
 aaacaaggga aaaaaattct attaaactcaa aaaatgaatg aaaatttt 1548

<210> 29  
 <211> 252

- 34 -

<212> DNA  
 <213> Staphylococcus epidermidis

<400> 29  
 ggtacaccat tagaattagt ttttgtcaat actttaggac ctaaaccttg tttcgctaaa 60  
 ccaaataaaa ttctactatt agaatatatt ccgctatttg ttgcagatgc tgctgctggt 120  
 aaaacaacaa aattaactat gccagcagca aagggaacac caattagtgt gaataattta 180  
 acaaacggac tactatcagg atcaacttta aaccatggaa tgacagacat gattacaagt 240  
 aaaccaccta ta 252

<210> 30  
 <211> 162  
 <212> DNA  
 <213> Staphylococcus epidermidis

<400> 30  
 tcatacgttaa gtaccataat tcctttttct ttaggagcat taggcaaatt taattctttc 60  
 attgagcaaa tcataccact agaatctacc ccacgtaatt gggcatcttt aattaccatt 120  
 ccgcttggca taacggcccc aacttttgca acaacgacct tc 162

<210> 31  
 <211> 348  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 31  
 atgaaattta aaaaatatat attaacagga acattagcat tactttttatc atcaactggg 60  
 atagcaacta tagaaggga taaagcagat gcaagtagtc tggacaaata tttaactgaa 120  
 agtcagtttc atgataaacg catagcagaa gaattaagaa ctttacttaa caaatcgaat 180  
 gtatatgcat tagctgcagg aagcttaa atccatattata aacgtacgat tatgatgaat 240  
 gaatatagag ctaaagcggc acttaagaaa aatgatttcg tatcaatggc tgatgctaaa 300  
 gttgcattag aaaaaatata caaagaaatt gatgaaatta taaataga 348

<210> 32  
 <211> 676  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 32

Met Lys Arg Thr Asp Lys Ile Gly Val Tyr Leu Lys Leu Ser Cys Ser  
 1 5 10 15

Ala Leu Leu Leu Ser Gly Ser Leu Val Gly Tyr Gly Phe Thr Lys Asp  
 20 25 30

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Ala Phe Ala Asp Ser Glu Ser Thr Ser Ser Asn Val Glu Asn Thr Ser  
           35                                  40                                  45

Asn Ser Asn Ser Ile Ala Asp Lys Ile Gln Gln Ala Lys Asp Asp Ile  
       50                                  55                                  60

Lys Asp Leu Lys Glu Leu Ser Asp Ala Asp Ile Lys Ser Phe Glu Glu  
   65                                  70                                  75                                  80

Arg Leu Asp Lys Val Asp Asn Gln Ser Ser Ile Asp Arg Ile Ile Asn  
                                   85                                  90                                  95

Asp Ala Lys Asp Lys Asn Asn His Leu Lys Ser Thr Asp Ser Ser Ala  
                                   100                                  105                                  110

Thr Ser Ser Lys Thr Glu Asp Asp Asp Thr Ser Glu Lys Asp Asn Asp  
                                   115                                  120                                  125

Asp Met Thr Lys Asp Leu Asp Lys Ile Leu Ser Asp Leu Asp Ser Ile  
       130                                  135                                  140

Ala Lys Asn Val Asp Asn Arg Gln Gln Gly Glu Glu Arg Ala Ser Lys  
   145                                  150                                  155                                  160

Pro Ser Asp Ser Thr Thr Asp Glu Lys Asp Asp Ser Asn Asn Lys Val  
                                   165                                  170                                  175

His Asp Thr Asn Ala Ser Thr Arg Asn Ala Thr Thr Asp Asp Ser Glu  
                                   180                                  185                                  190

Glu Ser Val Ile Asp Lys Leu Asp Lys Ile Gln Gln Asp Phe Lys Ser  
       195                                  200                                  205

Asp Ser Asn Asn Asn Pro Ser Glu Gln Ser Asp Gln Gln Ala Ser Pro  
       210                                  215                                  220

Ser Asn Lys Thr Glu Asn Asn Lys Glu Glu Ser Ser Thr Thr Thr Asn  
   225                                  230                                  235                                  240

Gln Ser Asp Ser Asp Ser Lys Asp Asp Lys Ser Asn Asp Gly His Arg  
                                   245                                  250                                  255

Ser Thr Leu Glu Arg Ile Ala Ser Asp Thr Asp Gln Ile Arg Asp Ser  
                                   260                                  265                                  270

Lys Asp Gln His Val Thr Asp Glu Lys Gln Asp Ile Gln Ala Ile Thr  
       275                                  280                                  285

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Arg Ser Leu Gln Gly Ser Asp Lys Ile Glu Lys Ala Leu Ala Lys Val  
 290 295 300

Gln Ser Asp Asn Gln Ser Leu Asp Ser Asn Tyr Ile Asn Asn Lys Leu  
 305 310 315 320

Met Asn Leu Arg Ser Leu Asp Thr Lys Val Glu Asp Asn Asn Thr Leu  
 325 330 335

Ser Asp Asp Lys Lys Gln Ala Leu Lys Gln Glu Ile Asp Lys Thr Lys  
 340 345 350

Gln Ser Ile Asp Arg Gln Arg Asn Ile Ile Ile Asp Gln Leu Asn Gly  
 355 360 365

Ala Ser Asn Lys Lys Gln Ala Thr Glu Asp Ile Leu Asn Ser Val Phe  
 370 375 380

Ser Lys Asn Glu Val Glu Asp Ile Met Lys Arg Ile Lys Thr Asn Gly  
 385 390 395 400

Arg Ser Asn Glu Asp Ile Ala Asn Gln Ile Ala Lys Gln Ile Asp Gly  
 405 410 415

Leu Ala Leu Thr Ser Ser Asp Asp Ile Leu Lys Ser Met Leu Asp Gln  
 420 425 430

Ser Lys Asp Lys Glu Ser Leu Ile Lys Gln Leu Leu Thr Thr Arg Leu  
 435 440 445

Gly Asn Asp Glu Ala Asp Arg Ile Ala Lys Lys Leu Leu Ser Gln Asn  
 450 455 460

Leu Ser Asn Ser Gln Ile Val Glu Gln Leu Lys Arg His Phe Asn Ser  
 465 470 475 480

Gln Gly Thr Ala Thr Ala Asp Asp Ile Leu Asn Gly Val Ile Asn Asp  
 485 490 495

Ala Lys Asp Lys Arg Gln Ala Ile Glu Thr Ile Leu Gln Thr Arg Ile  
 500 505 510

Asn Lys Asp Lys Ala Lys Ile Ile Ala Asp Val Ile Ala Arg Val Gln  
 515 520 525



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Lys Asp Lys Ser Asp Ile Met Asp Leu Ile His Ser Ala Ile Glu Gly  
 530 535 540

Lys Ala Asn Asp Leu Leu Asp Ile Glu Lys Arg Ala Lys Gln Ala Lys  
 545 550 555 560

Lys Asp Leu Glu Tyr Ile Leu Asp Pro Ile Lys Asn Arg Pro Ser Leu  
 565 570 575

Leu Asp Arg Ile Asn Lys Gly Val Gly Asp Ser Asn Ser Ile Phe Asp  
 580 585 590

Arg Pro Ser Leu Leu Asp Lys Leu His Ser Arg Gly Ser Ile Leu Asp  
 595 600 605

Lys Leu Asp His Ser Ala Pro Glu Asn Gly Leu Ser Leu Asp Asn Lys  
 610 615 620

Gly Gly Leu Leu Ser Asp Leu Phe Asp Asp Asp Gly Asn Ile Ser Leu  
 625 630 635 640

Pro Ala Thr Gly Glu Val Ile Lys Gln His Trp Ile Pro Val Ala Val  
 645 650 655

Val Leu Met Ser Leu Gly Gly Ala Leu Ile Phe Met Ala Arg Arg Lys  
 660 665 670

Lys His Gln Asn  
 675

<210> 33  
 <211> 655  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 33

Met Lys Lys Asn Lys Phe Leu Val Tyr Leu Leu Ser Thr Ala Leu Ile  
 1 5 10 15

Thr Pro Thr Phe Ala Thr Gln Thr Ala Phe Ala Glu Asp Ser Ser Asn  
 20 25 30

Lys Asn Thr Asn Ser Asp Lys Met Glu Gln His Gln Ser Gln Lys Glu  
 35 40 45

Thr Ser Lys Gln Ser Glu Lys Asp Glu Phe Asn Asn Asp Asp Ser Lys  
 50 55 60

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His Asp Ser Asp Asp Lys Lys Ser Thr Ser Asp Ser Lys Asp Lys Asp  
65 70 75 80

Ser Asn Lys Pro Leu Ser Ala Asp Ser Thr His Arg Asn Tyr Lys Met  
85 90 95

Lys Asp Asp Asn Leu Val Asp Gln Leu Tyr Asp Asn Phe Lys Ser Gln  
100 105 110

Ser Val Asp Phe Ser Lys Tyr Trp Glu Pro Asn Lys Tyr Glu Asp Ser  
115 120 125

Phe Ser Leu Thr Ser Leu Ile Gln Asn Leu Phe Asp Phe Asp Ser Asp  
130 135 140

Ile Thr Asp Tyr Glu Gln Pro Gln Lys Thr Ser His Ser Ser Asn Asp  
145 150 155 160

Glu Lys Asp Gln Val Asp Gln Ala Asp Gln Ala Lys Gln Pro Ser Gln  
165 170 175

His Gln Glu Pro Ser Gln Ser Ser Ala Lys Gln Asp Gln Glu Pro Ser  
180 185 190

Asn Asp Glu Lys Glu Lys Thr Thr Asn His Gln Ala Asp Ser Asp Val  
195 200 205

Ser Asp Leu Leu Gly Glu Met Asp Lys Glu Asp Gln Glu Gly Glu Asn  
210 215 220

Val Asp Thr Asn Lys Asn Gln Ser Ser Ser Glu Gln Gln Gln Thr Gln  
225 230 235 240

Ala Asn Asp Asp Ser Ser Glu Arg Asn Lys Lys Tyr Ser Ser Ile Thr  
245 250 255

Asp Ser Ala Leu Asp Ser Ile Leu Asp Glu Tyr Ser Gln Asp Ala Lys  
260 265 270

Lys Thr Glu Lys Asp Tyr Asn Lys Ser Lys Asn Thr Ser His Thr Lys  
275 280 285

Thr Ser Gln Ser Asp Asn Ala Asp Lys Asn Pro Gln Leu Pro Thr Asp  
290 295 300

Asp Glu Leu Lys His Gln Ser Lys Pro Ala Gln Ser Phe Glu Asp Asp

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305		310		315		320
Ile Lys Arg Ser	Asn Thr Arg Ser Thr Ser Leu Phe Gln Gln Leu Pro					
	325			330		335
Glu Leu Asp Asn Gly Asp Leu Ser Ser Asp Ser Phe Asn Val Val Asp						
	340			345		350
Ser Gln Asp Thr Arg Asp Phe Ile Gln Ser Ile Ala Lys Asp Ala His						
	355			360		365
Gln Ile Gly Lys Asp Gln Asp Ile Tyr Ala Ser Val Met Ile Ala Gln						
	370			375		380
Ala Ile Leu Glu Ser Asp Ser Gly Lys Ser Ser Leu Ala Gln Ser Pro						
	385			390		400
Asn His Asn Leu Phe Gly Ile Lys Gly Asp Tyr Lys Gly Gln Ser Val						
	405			410		415
Thr Phe Asn Thr Leu Glu Ala Asp Ser Ser Asn His Met Phe Ser Ile						
	420			425		430
Gln Ala Gly Phe Arg Lys Tyr Pro Ser Thr Lys Gln Ser Leu Glu Asp						
	435			440		445
Tyr Ala Asp Leu Ile Lys His Gly Ile Asp Gly Asn Pro Ser Ile Tyr						
	450			455		460
Lys Pro Thr Trp Lys Ser Glu Ala Leu Ser Tyr Lys Asp Ala Thr Ser						
	465			470		480
His Leu Ser Arg Ser Tyr Ala Thr Asp Pro Asn Tyr Ser Lys Lys Leu						
	485			490		495
Asn Ser Ile Ile Lys His Tyr His Leu Thr Ser Phe Asp Lys Glu Lys						
	500			505		510
Met Pro Asn Met Lys Lys Tyr Asn Lys Ser Ile Gly Thr Asp Val Ser						
	515			520		525
Gly Asn Asp Phe Lys Pro Phe Thr Glu Thr Ser Gly Thr Ser Pro Tyr						
	530			535		540
Pro His Gly Gln Cys Thr Trp Tyr Val Tyr His Arg Met Asn Gln Phe						
	545			550		560

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Asp Ala Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn Asn  
                   565                                  570                                  575

Arg Ala Glu Ser Glu Gly Tyr Thr Val Thr His Thr Pro Lys Asn His  
                   580                                  585                                  590

Thr Ala Val Val Phe Glu Ala Gly Gln Leu Gly Ala Asp Thr Gln Tyr  
                   595                                  600                                  605

Gly His Val Ala Phe Val Glu Lys Val Asn Asp Asp Gly Ser Ile Val  
                   610                                  615                                  620

Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Val Ile Ser Phe Arg Thr  
                   625                                  630                                  635                                  640

Ile Asp Ala Gly Asp Ala Gln Asp Leu Asp Tyr Ile Lys Gly Lys  
                                   645                                  650                                  655

<210> 34  
 <211> 164  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 34

Met Ile Arg Phe Ala Arg Leu Glu Asp Leu Gln Asp Ile Leu Thr Ile  
   1                  5                                  10                                  15

Tyr Asn Asp Ala Ile Leu Asn Thr Thr Ala Val Tyr Thr Tyr Lys Pro  
                   20                                  25                                  30

Gln Gln Leu Asp Glu Arg Leu Gln Trp Tyr Gln Ser Lys Ala Lys Ile  
                   35                                  40                                  45

Asn Glu Pro Ile Trp Val Tyr Glu Lys Glu Gly Lys Val Val Gly Phe  
                   50                                  55                                  60

Ala Thr Tyr Gly Ser Phe Arg Gln Trp Pro Ala Tyr Leu Tyr Thr Ile  
   65                                  70                                  75                                  80

Glu His Ser Ile Tyr Val His Gln Gln Tyr Arg Gly Leu Gly Ile Ala  
                   85                                  90                                  95

Ser Gln Leu Leu Glu Asn Leu Ile Arg Tyr Ala Lys Glu Gln Gly Tyr  
                   100                                  105                                  110

Arg Thr Ile Val Ala Gly Ile Asp Ala Ser Asn Met Asp Ser Ile Ala  
                   115                                  120                                  125

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Leu His Lys Lys Phe Asp Phe Ser His Ala Gly Thr Ile Lys Asn Val  
 130 135 140

Gly Tyr Lys Phe Asp Arg Trp Leu Asp Leu Ser Phe Tyr Gln Tyr Asp  
 145 150 155 160

Leu Ser Asp Ser

<210> 35  
 <211> 952  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 35

Leu Ser Asn Leu Ile Gln Asp Ile Lys Gln Ser Leu Tyr Lys Gly Phe  
 1 5 10 15

Ile Asp Lys Asp Ser Ser His Lys Gly Asn Phe Val Pro Arg Leu Leu  
 20 25 30

Val Asn Asn Lys Glu Glu Asn Val Leu Ser Thr Ile Ile Asp Gln Leu  
 35 40 45

His Asn Cys Gln Ser Phe Cys Ile Ser Val Ala Phe Ile Thr Glu Ser  
 50 55 60

Gly Leu Ala Ser Leu Lys Ser His Phe Tyr Asp Leu Ser Lys Lys Gly  
 65 70 75 80

Val Lys Gly Arg Ile Ile Thr Ser Asn Tyr Leu Gly Phe Asn Ser Pro  
 85 90 95

Lys Met Phe Glu Glu Leu Leu Lys Leu Glu Asn Val Glu Val Lys Leu  
 100 105 110

Thr Asn Ile Glu Gly Phe His Ala Lys Gly Tyr Ile Phe Glu His His  
 115 120 125

Asn His Thr Ser Phe Ile Ile Gly Ser Ser Asn Leu Thr Ser Asn Ala  
 130 135 140

Leu Lys Leu Asn Tyr Glu His Asn Leu Phe Leu Ser Thr His Lys Asn  
 145 150 155 160

Gly Asp Leu Val Asn Asn Ile Lys Tyr Lys Phe Asp Glu Leu Trp Asp

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165

170

175

Ser Ser Phe Ser Leu Thr Asn Glu Trp Ile Asn Glu Tyr Lys Gln Ser  
 180 185 190

Phe Glu Tyr Gln Thr Leu Gln Lys Val Phe Asp Asn Thr Val Val Gln  
 195 200 205

Asn Ser Asp Ile Lys Lys Phe Asn Glu Ser Lys Leu Ile Lys Pro Asn  
 210 215 220

Leu Met Gln Glu His Ala Leu Lys Ser Leu Glu Ser Leu Arg Asn Val  
 225 230 235 240

Gly Glu Glu Lys Gly Leu Ile Ile Ser Ala Thr Gly Thr Gly Lys Thr  
 245 250 255

Ile Leu Cys Ala Leu Asp Val Arg Ala Tyr Ser Pro Asp Lys Phe Leu  
 260 265 270

Phe Ile Val His Asn Glu Gly Ile Leu Asn Arg Ala Ile Glu Glu Phe  
 275 280 285

Lys Lys Val Phe Pro Tyr Glu Asp Glu Ser Asn Phe Gly Leu Leu Thr  
 290 295 300

Gly Lys Arg Lys Asp His Asp Ala Lys Phe Leu Phe Ala Thr Ile Gln  
 305 310 315 320

Thr Leu Ser Lys Lys Glu Asn Tyr Lys Leu Phe Asn Ser Asn His Phe  
 325 330 335

Asp Tyr Ile Val Phe Asp Glu Ala His Arg Ile Ala Ala Ser Ser Tyr  
 340 345 350

Gln Lys Ile Phe Asn Tyr Phe Lys Pro Asn Phe Leu Leu Gly Met Thr  
 355 360 365

Ala Thr Pro Glu Arg Thr Asp Glu Leu Asn Ile Phe Glu Leu Phe Asn  
 370 375 380

Tyr Asn Ile Ala Tyr Glu Ile Arg Leu Gln Glu Ala Leu Glu Ser Asn  
 385 390 395 400

Ile Leu Cys Pro Phe His Tyr Phe Gly Val Thr Asp Tyr Ile Gln Asn  
 405 410 415

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Glu Met Ser Gln Glu Asp Ala Phe Asn Leu Lys Tyr Leu Ala Ser Asn  
                   420                                  425                                  430

Glu Arg Val Glu His Ile Ile Lys Lys Thr Asn Tyr Tyr Gly Tyr Ser  
                   435                                  440                                  445

Gly Asp Val Leu Lys Gly Leu Ile Phe Val Ser Ser Arg Gly Glu Ala  
                   450                                  455                                  460

Tyr Gln Leu Ala Asn Gln Leu Ser Lys Arg Gly Ile Ser Ser Val Gly  
                   465                                  470                                  475                                  480

Leu Thr Gly Lys Asp Ser Ile Ala Tyr Arg Ala Glu Thr Ile Gln Gln  
                                   485                                  490                                  495

Leu Lys Glu Gly Ser Ile Asn Tyr Ile Ile Thr Val Asp Leu Phe Asn  
                                   500                                  505                                  510

Glu Gly Ile Asp Ile Pro Glu Ile Asn Gln Val Val Met Leu Arg Pro  
                   515                                  520                                  525

Thr Lys Ser Ser Ile Ile Phe Ile Gln Gln Leu Gly Arg Gly Leu Arg  
                   530                                  535                                  540

Lys Ser Thr Asn Lys Glu Phe Val Thr Val Ile Asp Phe Ile Gly Asn  
                   545                                  550                                  555                                  560

Tyr Lys Thr Asn Tyr Met Ile Pro Ile Ala Leu Ser Gly Asn Lys Ser  
                                   565                                  570                                  575

Gln Asn Lys Asp Asn Tyr Arg Lys Phe Leu Thr Asp Thr Thr Val Leu  
                                   580                                  585                                  590

Asn Gly Val Ser Thr Ile Asn Phe Glu Glu Val Ala Lys Asn Lys Ile  
                   595                                  600                                  605

Tyr Asn Ser Leu Asp Ser Val Lys Leu Asn Gln Pro Lys Leu Ile Lys  
                   610                                  615                                  620

Glu Ala Phe Asn Asn Val Lys Asp Arg Ile Gly Lys Leu Pro Leu Leu  
                   625                                  630                                  635                                  640

Met Asp Phe Ile Asn Asn Asp Ser Ile Asp Pro Ser Val Ile Phe Ser  
                                   645                                  650                                  655

Arg Phe Lys Asn Tyr Tyr Glu Phe Leu Ile Lys Asn Lys Ile Ile Glu

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660	665	670
Asn Glu Leu Ser Ile Asn Glu Phe Lys Asn Leu Thr Phe Leu Ser Arg 675 680 685		
Gln Leu Thr Pro Gly Leu Lys Lys Val Asp Ile Asp Val Leu Lys Glu 690 695 700		
Ile Ile Gln Asn Asp Val Thr Tyr Glu Asn Leu Thr Lys Lys Met Leu 705 710 715 720		
Asn Ile Asn Asn Asp Ile Ser Glu Tyr Asp Ile Asn Thr Ser Leu Ser 725 730 735		
Ile Leu Asp Phe Thr Phe Phe Lys Lys Thr Ile Gly Lys Thr Tyr Gly 740 745 750		
Leu Pro Leu Ile Gln Tyr Lys Asp Asn Leu Ile Cys Leu Ala Asn Glu 755 760 765		
Phe Lys Glu Ala Leu Asn Lys Pro Leu Phe Asn Thr Phe Ile His Asp 770 775 780		
Leu Ile Asp Leu Ala Asn Tyr Asn Asn Asp Arg Tyr Gln Asn Lys Lys 785 790 795 800		
Asn Ser Leu Ile Leu Tyr Asn Lys Tyr Ser Arg Glu Asp Phe Val Lys 805 810 815		
Leu Leu Asn Trp Asp Lys Asp Glu Ser Gly Thr Ile Asn Gly Tyr Arg 820 825 830		
Met Lys His Arg Thr Leu Pro Leu Phe Ile Thr Tyr Asp Lys His Glu 835 840 845		
Asn Ile Ser Asp Asn Thr Lys Tyr Asp Asp Glu Phe Leu Ser Gln Asp 850 855 860		
Glu Leu Lys Trp Tyr Thr Arg Ser Asn Arg Lys Leu Thr Ser Pro Glu 865 870 875 880		
Val Gln Asn Ile Leu Lys His Glu Glu Ser Asn Thr Asp Met Tyr Ile 885 890 895		
Phe Val Lys Lys Arg Asp Asp Glu Gly Lys Tyr Phe Tyr Tyr Leu Gly 900 905 910		



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Lys Ala Lys Tyr Ile Lys Gly Thr Glu Lys Gln Asp Tyr Met Pro Asn  
 915 920 925

Gly Asn Ser Val Val Thr Met His Leu Ser Met Asn Thr Ser Ile Arg  
 930 935 940

Asp Asp Ile Tyr Arg Tyr Ile Thr  
 945 950

<210> 36  
 <211> 325  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 36

Met Thr Lys Ser Gln Gln Lys Val Ser Ser Ile Glu Lys Leu Ser Asn  
 1 5 10 15

Gln Glu Gly Ile Ile Ser Ala Leu Ala Phe Asp Gln Arg Gly Ala Leu  
 20 25 30

Lys Arg Met Met Ala Glu His Gln Ser Glu Thr Pro Thr Val Glu Gln  
 35 40 45

Ile Glu Gln Leu Lys Val Leu Val Ser Glu Glu Leu Thr Gln Tyr Ala  
 50 55 60

Ser Ser Ile Leu Leu Asp Pro Glu Tyr Gly Leu Pro Ala Ser Asp Ala  
 65 70 75 80

Arg Asn Asn Asp Cys Gly Leu Leu Leu Ala Tyr Glu Lys Thr Gly Tyr  
 85 90 95

Asp Val Asn Ala Lys Gly Arg Leu Pro Asp Cys Leu Val Glu Trp Ser  
 100 105 110

Ala Lys Arg Leu Lys Glu Gln Gly Ala Asn Ala Val Lys Phe Leu Leu  
 115 120 125

Tyr Tyr Asp Val Asp Asp Thr Glu Glu Ile Asn Ile Gln Lys Lys Ala  
 130 135 140

Tyr Ile Glu Arg Ile Gly Ser Glu Cys Val Ala Glu Asp Ile Pro Phe  
 145 150 155 160

Phe Leu Glu Val Leu Thr Tyr Asp Asp Asn Ile Pro Asp Asn Lys Ser  
 165 170 175

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Ala Glu Phe Ala Lys Val Lys Pro Arg Lys Val Asn Glu Ala Met Lys  
 180 185 190

Leu Phe Ser Glu Asp Arg Phe Asn Val Asp Val Leu Lys Val Glu Val  
 195 200 205

Pro Val Asn Met Asn Phe Val Glu Gly Phe Ser Glu Gly Glu Val Val  
 210 215 220

Tyr Thr Lys Glu Glu Ala Ala Gln His Phe Arg Asp Gln Asp Ala Ala  
 225 230 235 240

Thr His Leu Pro Tyr Ile Tyr Leu Ser Ala Gly Val Ser Ala Glu Leu  
 245 250 255

Phe Gln Asp Thr Leu Lys Phe Ala His Asp Ser Gly Ala Gln Phe Asn  
 260 265 270

Gly Val Leu Cys Gly Arg Ala Thr Trp Ser Gly Ala Val Lys Val Tyr  
 275 280 285

Ile Glu Glu Gly Glu Gln Ala Ala Arg Glu Trp Leu Arg Thr Val Gly  
 290 295 300

Phe Lys Asn Ile Asp Asp Leu Asn Thr Val Leu Lys Thr Thr Ala Thr  
 305 310 315 320

Ser Trp Lys Asn Lys  
 325

<210> 37  
 <211> 382  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 37

Leu Met Lys Lys Val Met Thr Ile Phe Gly Thr Arg Pro Glu Ala Ile  
 1 5 10 15

Lys Met Ala Pro Leu Ile Lys Thr Leu Glu Lys Asp Ser Asp Leu Glu  
 20 25 30

Pro Val Val Val Val Thr Ala Gln His Arg Glu Met Leu Asp Ser Val  
 35 40 45

Leu Asn Thr Phe Asn Ile Ser Ala Asp Tyr Asp Leu Asn Ile Met Lys

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50

55

60

Ala Gly Gln Thr Leu Ser Glu Val Thr Ser Glu Ala Met Lys Lys Leu  
 65 70 75 80

Glu Asp Ile Ile Gln Lys Glu Val Pro Asp Met Val Leu Val His Gly  
 85 90 95

Asp Thr Val Thr Thr Phe Ser Gly Ala Leu Ala Ala Phe Tyr Ser Gln  
 100 105 110

Thr Pro Ile Gly His Val Glu Ala Gly Leu Arg Ser Tyr Asn Lys Tyr  
 115 120 125

Ser Pro Tyr Pro Glu Glu Ile Asn Arg Gln Met Val Gly Val Met Ala  
 130 135 140

Asp Leu His Phe Ala Pro Thr Tyr Asn Ala Ala Gln Asn Leu Val Lys  
 145 150 155 160

Glu Gly Lys Leu Ala Lys His Ile Ala Ile Thr Gly Asn Thr Ala Ile  
 165 170 175

Asp Ala Met Asn Tyr Thr Ile Asp His Gln Tyr Ser Ser Ser Ile Ile  
 180 185 190

Gln Lys His Lys Asn Lys Asn Phe Ile Leu Leu Thr Ala His Arg Arg  
 195 200 205

Glu Asn Ile Gly Lys Pro Met Ile Asn Val Phe Lys Ala Ile Arg Lys  
 210 215 220

Leu Ile Asp Glu Tyr Gln Asp Leu Ala Leu Val Tyr Pro Met His Met  
 225 230 235 240

Asn Pro Lys Val Arg Asp Ile Ala Gln Lys Tyr Leu Gly Asn His Pro  
 245 250 255

Arg Ile Glu Leu Ile Glu Pro Leu Asp Val Val Asp Phe His Asn Phe  
 260 265 270

Ala Lys Gln Ala Tyr Leu Ile Met Thr Asp Ser Gly Gly Ile Gln Glu  
 275 280 285

Glu Ala Pro Ser Leu His Lys Pro Val Leu Val Leu Arg Asp Ser Thr  
 290 295 300

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Glu Arg Pro Glu Gly Val Asp Ala Gly Thr Leu Arg Val Ile Gly Thr  
 305 310 315 320

Asn Glu Glu Asp Val Tyr Asn Glu Thr Lys Lys Leu Ile Glu Asn Pro  
 325 330 335

Asp Leu Tyr Gln Lys Met Ser Gln Ala Val Asn Pro Tyr Gly Asp Gly  
 340 345 350

Gln Ala Ser Glu Arg Ile Val Gln His Ile Lys Tyr Tyr Phe Asn Leu  
 355 360 365

Thr Asn Asp Arg Pro Asn His Phe Glu Phe Thr Lys Asp Leu  
 370 375 380

<210> 38  
 <211> 2757  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 38

Val Ala Ser Asp Phe Asn Ile Gly Ile Leu Ser Thr Leu Glu Ile Asp  
 1 5 10 15

Ser Ser Ser Ser Arg Lys Lys Ile Asn Asp Thr Leu Lys Asn Ile Glu  
 20 25 30

Ala Asn Ile Asn Ser Ile Lys Ala Asp Leu Glu Val Ser Asp Thr Lys  
 35 40 45

Lys Ser Glu Asn Asn Ala Ile Lys Ser Ala Asn Asn Val Ile Arg Asn  
 50 55 60

Ile Asn Ser Asn Gly Asn Leu Lys Lys Leu Asn Val Glu Leu Asp Val  
 65 70 75 80

Asn Leu Thr Lys Ser Arg Gln Asn Ile Gln Arg Ala Leu Ser Thr Leu  
 85 90 95

Ser Lys Asp Phe Lys Asn Lys Lys Ile Asp Val Glu Val Asn Ala Lys  
 100 105 110

Ala Asn Lys Asn Ser Ile Gly Gln Val Lys Asn Ser Ile Ser Lys Gly  
 115 120 125

Ala Ser Gln Pro Leu Glu Ile Lys Glu Ser Pro Ser Ser Arg Ser Thr  
 130 135 140

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Ser Arg Asp Ile Lys Glu Gln Gln Ser Leu Met Thr Gly Leu Ala Asn  
 145 150 155 160

Ser Tyr Lys Asn Leu Asp Asp Leu Thr Arg Ala Leu Asn Thr Ser Thr  
 165 170 175

Phe Glu Gly Leu Arg Lys Thr Val Lys Glu Ile Lys Asn Ala Asp Asn  
 180 185 190

Ser Leu Lys Ser Tyr Gln Val Thr Leu Glu Arg Val Asn Gln Glu Gly  
 195 200 205

Lys Lys Leu Gly Ser Gln Arg Phe Asp Tyr Thr Pro Ser Ala Asn Gly  
 210 215 220

Leu Lys Leu Asn Lys Thr Gln Leu Thr Asp Gln Thr Asp Lys Ala Arg  
 225 230 235 240

Lys Glu Glu Asn Ala Ala Ile Asn Lys Leu Leu Glu Asn Glu Val Ser  
 245 250 255

Lys Tyr Asp Arg Leu Leu Asn Lys Gly Lys Ile Asp Ile Lys Gln His  
 260 265 270

Gln Thr Leu Leu Gln Thr Leu Arg Gln Ile Thr Asn Glu Lys Ser Lys  
 275 280 285

Ala Asn Gln Phe Asn Arg Thr Asp Phe Asn Arg Val Ala Lys Ala Ala  
 290 295 300

Ala Asp Glu Ala Lys Glu Tyr Gln Tyr Gln Asn Asp Met Leu Arg Lys  
 305 310 315 320

Lys Leu Ala Leu Thr Ser Gln Ile Glu Arg Ile Glu Asn Arg Met Ala  
 325 330 335

Ala Thr Ile Asp Lys Gln Gln Thr Asn Ala Leu Lys Asn Gln Leu Asn  
 340 345 350

Ser Leu Gly Asn Asn Arg Thr Pro Phe Gly Lys Glu Ala Ala Phe His  
 355 360 365

Met Asn Gln Ile Gln Asp Lys Val Arg Gln Ile Ser Ala Glu Ala Glu  
 370 375 380

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Arg Ala Thr Arg Thr Gln Leu Ser Phe Val Asp Gln Phe Arg Glu Ala  
 385 390 395 400

Met Thr Lys Phe Pro Val Trp Met Gly Ala Thr Thr Leu Phe Phe Gly  
 405 410 415

Ala Ile Asn Gly Ala Lys Glu Met Leu Asp Val Ile Thr Glu Ile Asp  
 420 425 430

Gly Lys Met Ile Thr Leu Ala Lys Val Thr Gly Asp Asp Asn Ala Leu  
 435 440 445

Gln Gln Thr Phe Ile Asp Ala Asn Asn Ala Ala Ser Gln Phe Gly Gln  
 450 455 460

Thr Leu Gly Ser Val Leu Asp Val Tyr Ala Glu Phe Ala Arg Gln Gly  
 465 470 475 480

Val Lys Gly Asn Glu Leu Ser Gln Phe Ser Asn Ala Ala Leu Ile Ala  
 485 490 495

Ala Asn Val Gly Glu Ile Asp Ala Lys Gln Ala Ser Glu Tyr Leu Thr  
 500 505 510

Ser Met Ser Ala Gln Trp Glu Thr Thr Gly Asn Gln Ala Met Arg Gln  
 515 520 525

Val Asp Ser Leu Asn Glu Val Ser Asn Lys Tyr Ala Thr Thr Val Glu  
 530 535 540

Lys Leu Ala Gln Gly Gln Ala Lys Ala Gly Ser Thr Ala Lys Ser Met  
 545 550 555 560

Gly Leu Thr Phe Asp Glu Thr Asn Gly Ile Ile Gly Ala Leu Thr Ala  
 565 570 575

Lys Thr Lys Gln Ser Gly Asp Glu Ile Gly Asn Phe Met Lys Ala Thr  
 580 585 590

Leu Pro Lys Leu Tyr Ser Gly Lys Gly Lys Ser Thr Ile Glu Gly Leu  
 595 600 605

Gly Ile Ser Met Lys Asp Glu Asn Gly Gln Leu Lys Ser Ala Ile Ser  
 610 615 620

Leu Leu Glu Glu Val Ser Gln Lys Thr Lys Asn Leu Glu Lys Asp Gln  
 625 630 635 640

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Lys Ala Ala Val Ile Asn Gly Leu Gly Gly Thr Tyr His Tyr Gln Arg  
                   645                                  650                                  655

Met Gln Val Leu Leu Asp Asp Leu Ser Lys Thr Asp Gly Leu Tyr Lys  
                   660                                  665                                  670

Gln Ile Lys Glu Ser Ser Glu Ser Ser Ala Gly Ser Ala Leu Gln Glu  
                   675                                  680                                  685

Asn Ala Lys Tyr Met Glu Ser Ile Glu Ala Lys Val Asn Gln Ala Lys  
                   690                                  695                                  700

Thr Ala Phe Glu Gln Phe Ala Leu Ala Val Gly Glu Thr Phe Ala Lys  
   705                                  710                                  715                                  720

Ser Gly Met Leu Asp Gly Ile Arg Met Val Thr Gln Leu Leu Thr Gly  
                   725                                  730                                  735

Leu Thr His Gly Ile Thr Glu Leu Gly Thr Thr Ala Pro Ile Phe Gly  
                   740                                  745                                  750

Met Val Gly Gly Ala Ala Ser Leu Met Ser Lys Asn Val Arg Ser Gly  
                   755                                  760                                  765

Phe Glu Gly Ala Arg Ser Ser Val Ala Asn Tyr Ile Thr Glu Val Asn  
   770                                  775                                  780

Lys Leu Ala Lys Val Asn Asn Ala Ala Gly Gln Val Val Gly Leu Gln  
   785                                  790                                  795                                  800

Lys Val Gln Thr Gly Thr Ala Ser Gln Leu Gln Phe Asn Lys Asn Gly  
                   805                                  810                                  815

Glu Tyr Asp Lys Ala Ala Ser Gln Ala Lys Ala Ala Glu Gln Ala Thr  
                   820                                  825                                  830

Tyr Gln Phe Ser Lys Ala Gln Lys Asp Val Ser Ala Ser Ala Met Ile  
                   835                                  840                                  845

Ala Ser Gly Ala Ile Asn Lys Thr Thr Val Ala Thr Thr Ala Ser Thr  
                   850                                  855                                  860

Val Ala Thr Arg Ala Ala Thr Leu Ala Val Asn Gly Leu Lys Leu Ala  
   865                                  870                                  875                                  880

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Phe Arg Gly Leu Leu Ala Ala Thr Gly Val Gly Leu Ala Ile Thr Gly  
                   885                  890                  895

Val Ser Phe Val Leu Glu Lys Val Val Gly Ser Phe Asn Ala Ala Ser  
                   900                  905                  910

Gln Ala Ala Glu Gln Tyr Lys Gln Lys Gln Glu Gln Thr Lys Gln Ala  
                   915                  920                  925

Ile Ala Ser Met Ser Asn Gly Glu Ile Asn Ser Leu Ile Ser Ser Tyr  
                   930                  935                  940

Asp Lys Leu Gln Gln Lys Met Asn Ser Gly Ser Ala Phe Asn Thr Ala  
                   945                  950                  955                  960

Glu Ala Glu Lys Tyr Lys Glu Val Thr Ser Gln Leu Ala Asn Ile Phe  
                   965                  970                  975

Pro Asp Leu Val Thr Gly Glu Asn Arg Tyr Gly Lys Glu Met Ala Gly  
                   980                  985                  990

Asn Lys Glu Val Met Lys Gln Lys Ile Glu Leu Ile Lys Gln Glu Met  
                   995                  1000                  1005

Glu Leu Glu Arg Gln Lys Asn Ala Ile Lys Gln Lys Glu Glu Gln  
                   1010                  1015                  1020

Asp Ala Tyr Ile Lys Glu Gln Asp Ser Leu Ala Lys Lys Asn Arg  
                   1025                  1030                  1035

Gly Gln Lys Trp Tyr Gln Leu Gly Gln Thr Pro Glu Leu Lys Leu  
                   1040                  1045                  1050

Gln Glu Gln Ala Arg Pro Thr Thr Val Ser Asp Asn Ser Asn Ile  
                   1055                  1060                  1065

Asn Lys Ile Asn Ala Thr Ile Gln Lys Val Lys Ser Gln Ala Gln  
                   1070                  1075                  1080

Ala Glu Lys Ala Leu Glu Gln Val Asp Lys Gln Leu Ala Gln Ser  
                   1085                  1090                  1095

Gln Thr Lys Asn Arg Gln Asn Glu Val Gln His Leu Gln Lys Val  
                   1100                  1105                  1110

Arg Gln Ala Leu Gln Asp Tyr Ile Thr Lys Thr Gly Gln Ala Asn  
                   1115                  1120                  1125



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Gln	Ala	Thr	Arg	Ala	Ala	Val	Leu	Thr	Ala	Gln	Gln	Gln	Phe	Thr
1130						1135					1140			
Asn	Gln	Ile	Ala	Thr	Met	Lys	Lys	Leu	Gly	Thr	Thr	Gly	Gln	Gln
1145						1150					1155			
Val	Met	Thr	Thr	Ile	Ser	Asn	Ser	Val	Ala	Lys	Thr	Ala	Lys	Ser
1160						1165					1170			
Gly	Lys	Ala	Ala	Gln	Ala	Thr	Phe	Lys	Ser	Phe	Glu	Thr	Ser	Leu
1175						1180					1185			
Val	Lys	Ser	Ser	Ser	Phe	Lys	Ser	Lys	Met	Ala	Ser	Tyr	Glu	Ala
1190						1195					1200			
Ser	Val	Lys	Lys	Phe	Lys	Asn	Ala	Ala	Asn	Gln	Ser	Ala	Lys	Ile
1205						1210					1215			
Ala	Ala	Leu	Lys	Asp	Val	Glu	Arg	Asp	Tyr	Ser	Lys	Val	Ala	Lys
1220						1225					1230			
Gly	Ile	Met	Gln	Ala	Ala	Lys	Ala	Ala	Asn	Met	Ser	Lys	Ser	Gln
1235						1240					1245			
Met	Lys	Asp	Leu	Lys	Lys	Ser	Leu	Gln	Gln	Asn	Ile	Gln	Ala	Glu
1250						1255					1260			
Thr	Gly	Phe	Arg	Ala	Ser	Val	Ser	Lys	Ala	Gly	Lys	Val	Thr	Ile
1265						1270					1275			
Asp	Gln	Ser	Lys	Lys	Ile	Lys	Gln	Asn	Thr	Ala	Glu	Thr	Arg	Arg
1280						1285					1290			
Asn	Ser	Ser	Ala	Lys	Leu	Gln	Asn	Ala	Asp	Ala	Ser	Asp	Gln	Ala
1295						1300					1305			
Ser	Glu	Glu	Asn	Lys	Glu	Leu	Ala	Asp	Ser	Met	Arg	Ala	Gly	Ile
1310						1315					1320			
Glu	Ser	Ser	Gln	Leu	Leu	Gly	Lys	Ala	Met	Gly	Glu	Leu	Gln	Ser
1325						1330					1335			
Gln	Gly	Thr	Leu	Ser	Thr	Glu	Thr	Leu	Ile	Glu	Leu	Thr	Glu	Lys
1340						1345					1350			

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Tyr	Gly	Asp	Glu	Ile	Leu	Ala	Val	Ala	Gly	Asp	Gln	Glu	Ala	Leu
	1355					1360					1365			
Ser	Asn	Phe	Ile	Met	Gln	Lys	Gln	Asn	Glu	Glu	Thr	Asp	Asn	Tyr
	1370					1375					1380			
Asn	Lys	Asn	Leu	Lys	Thr	Lys	Leu	Glu	Asn	Ser	Ser	Ser	Tyr	Tyr
	1385					1390					1395			
Lys	Ala	Val	Ala	Gly	Ala	Asp	Ser	Ala	Leu	Ser	Asn	Tyr	Leu	Met
	1400					1405					1410			
Glu	Asn	Tyr	Gly	Ile	Asp	Thr	Lys	Asn	Tyr	Lys	Ser	Leu	Thr	Glu
	1415					1420					1425			
Val	Lys	Ala	Lys	Ile	Thr	Asp	Leu	Tyr	Tyr	Asn	Gly	Ser	Ala	Glu
	1430					1435					1440			
Glu	Gln	Ala	Lys	Val	Val	Asp	Ala	Ile	Ala	Lys	Ala	Tyr	His	Ile
	1445					1450					1455			
Asp	Leu	Ser	Asn	Tyr	Gly	Ser	Leu	Asn	Glu	Lys	Lys	Glu	Ala	Leu
	1460					1465					1470			
Glu	Asn	Gln	Leu	Met	Lys	Ile	Leu	Gly	Ser	Lys	Trp	Lys	Lys	Tyr
	1475					1480					1485			
Ile	Gly	Ser	Val	Ala	Lys	Asp	Met	Lys	Ser	Leu	Gly	Val	Asp	Ala
	1490					1495					1500			
Gly	Glu	Val	Gly	Ala	Asp	Gly	Phe	Asp	Asp	Ser	Lys	Met	Phe	Asn
	1505					1510					1515			
Pro	Gly	Ala	Leu	Ile	Gly	Ala	Asn	Asn	Phe	Gln	Asn	Val	Ser	Asn
	1520					1525					1530			
Leu	Ser	Asn	Ile	Ser	Asn	Val	Phe	Asn	Ser	Leu	Asn	Gly	Ala	Phe
	1535					1540					1545			
Asn	Glu	Ala	Lys	Asn	Glu	Ala	Ala	Gly	Val	Ser	Arg	Gly	Leu	Asp
	1550					1555					1560			
Asp	Ala	Ala	Ser	Gly	Leu	Lys	Asp	Val	Gly	Asp	Ser	Ala	Gly	Ser
	1565					1570					1575			
Ala	Gly	Ser	Gly	Leu	Gly	Lys	Thr	Ala	Lys	Gly	Ala	Asp	Lys	Ala
	1580					1585					1590			

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Ser	Asp	Ser	Leu	Asp	Gly	Thr	Asn	Lys	Glu	Leu	Glu	Lys	Thr	Lys
1595						1600					1605			
Glu	Lys	Ala	Glu	Glu	Ala	Gly	Val	Thr	Val	Lys	Gln	Leu	Tyr	Lys
1610						1615					1620			
Gln	Phe	Thr	Val	Thr	Thr	Tyr	Val	Ala	Asp	Lys	Leu	Ser	Met	Ala
1625						1630					1635			
Leu	Asp	Lys	Ile	Asn	Asn	Lys	Leu	Glu	Lys	Gln	Lys	Leu	Leu	Thr
1640						1645					1650			
Glu	Lys	Tyr	Ala	Thr	Trp	Ser	Ser	Ser	Tyr	Arg	Asn	Ser	Leu	Lys
1655						1660					1665			
Ala	Glu	Asn	Lys	Leu	Leu	Asp	Glu	Lys	Thr	Ala	Lys	Ile	Lys	Lys
1670						1675					1680			
Gln	Ile	Glu	Ser	Met	Lys	Glu	Gln	Ile	Ala	Gln	Gly	Lys	Val	Ile
1685						1690					1695			
Glu	Tyr	Gly	Leu	Val	Gly	Lys	Asp	Ile	Asn	Val	Pro	Tyr	Tyr	Glu
1700						1705					1710			
Tyr	Thr	Ala	Asn	Asn	Leu	Asp	Asp	Gly	Glu	Thr	Gly	Arg	Ile	Ser
1715						1720					1725			
Arg	Tyr	Thr	Gly	Asn	Ser	Thr	Gln	Ala	Lys	Val	Trp	Asn	Phe	Phe
1730						1735					1740			
Lys	Ser	Lys	Gly	Leu	Ser	Asp	His	Ala	Val	Ala	Gly	Ile	Met	Gly
1745						1750					1755			
Asn	Met	Glu	Arg	Glu	Ser	Arg	Phe	Lys	Pro	Gly	Ala	Gln	Glu	Gln
1760						1765					1770			
Gly	Gly	Thr	Gly	Ile	Gly	Leu	Val	Gln	Leu	Ser	Phe	Gly	Arg	Ala
1775						1780					1785			
Asn	Asn	Leu	Arg	Asn	Tyr	Ala	Ala	Arg	Arg	Gly	Lys	Ser	Trp	Lys
1790						1795					1800			
Asp	Leu	Asn	Thr	Gln	Leu	Asp	Phe	Ile	Trp	Lys	Glu	Leu	Asn	Thr
1805						1810					1815			

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Thr	Glu	Val	Asn	Ala	Leu	Arg	Gly	Leu	Lys	Ser	Ala	Thr	Ser	Val
1820						1825					1830			
Ile	Gly	Ala	Ala	Asn	Ser	Phe	Gln	Arg	Leu	Tyr	Glu	Arg	Ala	Gly
1835						1840					1845			
Val	Val	Ala	Gln	Gly	Glu	Arg	Asn	Ala	Ala	Ala	Lys	Lys	Tyr	Tyr
1850						1855					1860			
Arg	Gln	Phe	Lys	Gly	Thr	Asn	Gly	Ser	Ser	Gly	Phe	Leu	Ser	Gly
1865						1870					1875			
Gly	Val	Val	Ala	Gly	Thr	Asn	Gly	Lys	Pro	Leu	Thr	Ser	Asp	Arg
1880						1885					1890			
Asn	Ala	Tyr	Ile	Leu	Asp	Arg	Gln	Phe	Gly	Arg	Tyr	Asn	Gly	Gly
1895						1900					1905			
Gly	Val	His	His	Gly	Arg	Asp	Ile	Thr	Ser	Ala	Thr	Ile	Asn	Gly
1910						1915					1920			
Ser	Pro	Ile	Lys	Ala	Ala	Arg	Ser	Gly	Ile	Val	Thr	Phe	Lys	Gly
1925						1930					1935			
Trp	Thr	Gly	Gly	Gly	Asn	Thr	Leu	Ser	Ile	Phe	Asp	Gly	Lys	Asn
1940						1945					1950			
Thr	Tyr	Thr	Tyr	Met	His	Met	Lys	Asn	Pro	Ala	Arg	Val	Val	Lys
1955						1960					1965			
Gly	Gln	Arg	Val	Lys	Ala	Gly	Gln	Ile	Val	Gly	Asn	Val	Gly	Thr
1970						1975					1980			
Thr	His	Asp	Arg	Arg	Leu	Gly	Gly	Phe	Ser	Thr	Gly	Pro	His	Leu
1985						1990					1995			
His	Val	Gln	Val	Asn	Leu	Gly	Lys	Thr	Pro	Ser	Gly	Thr	Phe	Met
2000						2005					2010			
Asn	Thr	Phe	Asn	Gly	Ala	His	Arg	Ala	Val	Asp	Pro	Val	Lys	Tyr
2015						2020					2025			
Gly	Tyr	Thr	Arg	Val	Ser	Gly	Gly	Gly	Ser	Leu	Asn	Leu	Gly	Ser
2030						2035					2040			
Leu	Thr	Ser	Gly	His	Ser	Ala	Met	Ser	Gly	Ser	Ile	Ser	Ala	Ala
2045						2050					2055			

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Met	Ala	Glu	Asp	Leu	Asn	Glu	Ala	Glu	Gln	Glu	Arg	Leu	Asn	Lys
2060						2065					2070			
Ile	Glu	Gln	Ala	Ile	Asn	Ala	His	Asn	Lys	Ala	Glu	Glu	Met	Lys
2075						2080					2085			
Gln	Lys	Val	Asp	Glu	Leu	Arg	Lys	Thr	Leu	Met	Asp	Lys	Gln	Leu
2090						2095					2100			
Glu	Glu	Val	Gln	Thr	Ala	Lys	Glu	Lys	Ser	Glu	Asn	Leu	Tyr	Asn
2105						2110					2115			
Ile	Gln	Lys	Ser	His	Val	Glu	Glu	Tyr	Asp	His	Trp	Arg	Thr	Leu
2120						2125					2130			
Gln	Glu	Ala	Arg	Ser	Ala	Lys	Leu	Glu	Tyr	Glu	Leu	Asn	Lys	Ile
2135						2140					2145			
Glu	Phe	Glu	Lys	Gly	Arg	Asn	Thr	Lys	Glu	Trp	Arg	Asn	Lys	Asn
2150						2155					2160			
Lys	Gln	Leu	Gln	Ala	Ser	Arg	Gln	Leu	Glu	Val	Asn	Phe	Glu	Asp
2165						2170					2175			
Ser	Lys	Ile	Gln	Tyr	Ile	Asn	Lys	Ala	Leu	Lys	Lys	Asn	Ala	Asn
2180						2185					2190			
Lys	Ile	Phe	Gly	Lys	Asn	Thr	Val	Asn	Arg	Asp	Glu	Phe	Glu	Thr
2195						2200					2205			
Met	Lys	Arg	Asp	Ala	Gln	Gln	Asn	Ile	Arg	Asp	Leu	Lys	Ala	Gly
2210						2215					2220			
Ile	Gln	Thr	Ala	Ser	Gly	Glu	Ile	Ala	Thr	Ser	Met	Ile	Asp	Gln
2225						2230					2235			
Ile	Leu	Asp	Glu	Tyr	Glu	Asp	Arg	Val	Gly	Lys	Val	Ser	Ala	Lys
2240						2245					2250			
Ile	Glu	Lys	Met	Gly	Lys	Gln	Lys	Glu	Lys	Leu	Asp	Leu	Ala	Asp
2255						2260					2265			
Asn	Lys	Gln	Ala	Leu	Lys	Ser	Ser	Ser	Leu	Ser	Arg	Gln	Gln	Ala
2270						2275					2280			

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Lys	Asp	Ser	Lys	Ser	Leu	Ala	Ser	Tyr	Ile	Asn	Phe	Tyr	Ile	Lys
2285						2290					2295			
Gln	Leu	Glu	Arg	Gln	Leu	Lys	Leu	Thr	Gly	Lys	Asn	His	Glu	Leu
2300						2305					2310			
Gln	Gln	Lys	Val	Lys	Glu	Gln	Ile	Lys	Glu	Met	Lys	Val	Ala	Tyr
2315						2320					2325			
Asp	Asp	Ala	Thr	Leu	Ala	Ala	His	Gln	Tyr	Ile	Thr	Glu	Ala	Ala
2330						2335					2340			
Glu	Val	Asp	Thr	Glu	Arg	Gln	Leu	Gln	Leu	Asn	Ala	Asn	Arg	Leu
2345						2350					2355			
Arg	Asp	Ala	Gln	Asn	Glu	Leu	Ser	Lys	Ala	Asp	Tyr	Lys	Ala	Gly
2360						2365					2370			
Phe	Ile	Ser	Gln	Glu	Tyr	Gln	Ile	Asp	Leu	Tyr	Arg	Lys	Asn	Gln
2375						2380					2385			
Glu	Ala	Lys	Phe	Lys	Gly	Tyr	Leu	Lys	Glu	Lys	Glu	Ala	Leu	Glu
2390						2395					2400			
Gln	Asn	Lys	Ser	Glu	Leu	Gln	Asp	Met	Tyr	Glu	Ile	Tyr	Lys	Ser
2405						2410					2415			
Val	Pro	Thr	Gln	Ala	Gln	Lys	Ile	Lys	Glu	Ala	Leu	Ile	Glu	Thr
2420						2425					2430			
Lys	Asn	Ala	Ile	Arg	Asp	Asn	Asn	Lys	Gly	Leu	Tyr	Asp	Leu	Lys
2435						2440					2445			
Tyr	Asp	Met	Ala	Asn	Ser	Val	Ile	Asn	Gln	Ile	Lys	Asp	Ile	Tyr
2450						2455					2460			
Ser	Lys	Gln	Leu	Glu	Val	Ala	Thr	Lys	Ala	Tyr	Asp	Asp	Glu	Tyr
2465						2470					2475			
Lys	Ala	Tyr	Glu	Lys	Met	Ile	Asn	Lys	Lys	Leu	Lys	Leu	Ile	Asp
2480						2485					2490			
Asp	Glu	Gln	Thr	Gln	Glu	Ser	Phe	Asn	Lys	Asp	Val	Arg	Asp	Arg
2495						2500					2505			
Thr	Glu	Ala	Met	Asp	Lys	Ile	Arg	Asp	Glu	Ile	Ala	Gln	Arg	Ser
2510						2515					2520			

Gly Asp 2525	Asp Ser Leu Ala Asn 2530	Gln Lys Lys Leu Lys 2535	Asp Leu Arg
Glu Gln 2540	Leu Lys Gln Gln Glu 2545	Glu Asp Tyr Thr Met 2550	Phe Ile Asn
Asn Lys 2555	Asn Arg Asp Asp Arg 2560	Arg Lys Ala Leu Gln 2565	Asp Glu Leu
Asn Asp 2570	Lys Asn Glu Gln Ile 2575	Gln Glu Gln Lys Glu 2580	Asp Leu Asn
Lys Ala 2585	Phe Gln Asp Leu Ile 2590	Gly Asp Thr Arg Arg 2595	Phe Asn Ala
Ile Gln 2600	Glu Ser Leu Met Glu 2605	Gly Gln Ile Asp Lys 2610	Tyr Lys Ser
Leu Ile 2615	Ala Asp Leu Thr Lys 2620	Tyr Val Asn Asp Asn 2625	Met Lys Glu
Ile Gly 2630	Arg Ser Thr Ser Glu 2635	Gly Ile Leu Asp Gly 2640	Leu Ala Ala
Ser Phe 2645	Lys Gly Leu Ser Ser 2650	Leu Ser Lys Glu Leu 2655	Gln Lys Gln
Glu Lys 2660	Asn Asn Leu Asn Pro 2665	Val Pro Asn Ser Lys 2670	Leu Lys Pro
Thr Lys 2675	Val Asp Glu Ala Thr 2680	Ile Ala Ala Ile Lys 2685	Lys Val Asn
Gly Leu 2690	Ser Pro Thr Thr Ile 2695	Leu Gln Gly Leu Asp 2700	Ile Lys Pro
Val Asn 2705	Leu Pro Lys Asp Val 2710	Lys Pro Ser Lys Thr 2715	Val Thr Asn
Asn Asn 2720	Lys Thr Thr Ala Lys 2725	Ala Leu Val Asn Ile 2730	Glu Asn Phe
Asn Gly 2735	Thr Lys Ala Glu Ala 2740	Asp Lys Leu Ala Asn 2745	Asn Leu Ala

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Thr Ala Met Arg Lys Gln Gly Val Leu  
 2750 2755

<210> 39  
 <211> 319  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 39

Met Ala Glu Thr Lys Lys Gln Phe Glu Asn Lys Val Ser Val Thr Gly  
 1 5 10 15

Thr Leu Lys Ser Leu Glu Val Thr Asp Leu Val Thr Ala Lys Lys Val  
 20 25 30

Pro Met Lys Ile Ala Thr Leu Arg Ile Glu Thr Gly Lys Gly Glu Thr  
 35 40 45

His Thr Ala Lys Met Met Ala Val Lys His Phe Glu Arg Asp Gly Val  
 50 55 60

Lys Thr Glu Asn Lys Ser Tyr Ser Ala Ile Glu Thr Met Gln Lys Glu  
 65 70 75 80

Tyr Val Ser Ile Glu Asp Ile Ser Glu Asn Lys Ala Gly Glu Asp Ala  
 85 90 95

Glu Ala Thr Val Val Asn Val Asn Gly Ser Met Ser Ile Asn Met Tyr  
 100 105 110

Lys Asn Lys Ala Glu Lys Val Val Glu Thr Asn Gln Ile Glu Ala Arg  
 115 120 125

Phe Val Asn Arg Val Lys Asp Val Glu Asn Ala Gln Phe Gly Ala Glu  
 130 135 140

Phe Thr Leu Gln Thr Tyr Leu Ile Ser Lys Gly Gln Arg Val Ile Lys  
 145 150 155 160

Asn Glu Glu Glu Thr Asp Glu Val Thr Phe Lys Ala Ala Thr Ile Asp  
 165 170 175

Tyr Arg Gly Gln Ala His Pro Phe Glu Phe Thr Ala Asn Asp Glu Tyr  
 180 185 190

Gly Val Ala Glu Trp Ile Glu Asp Glu Val Glu Leu Gly Gln Ser Leu  
 195 200 205



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Ile Leu Gln Gly Leu Ile Ile Asn Lys Phe Ile Val Glu Gln Val Glu  
 210 215 220

Arg Ser Ser Ser Ala Gly Ile Gly Lys Ala Ile Val Asp Thr Arg Arg  
 225 230 235 240

Glu Val Glu Arg Lys Leu Leu Val Glu Gly Ile Ile Pro Ile Glu Asp  
 245 250 255

Glu Asp Asp Pro Lys Tyr Ile Thr Glu Glu Glu Ile Lys Glu Ala Asn  
 260 265 270

Lys Lys Tyr Glu Asp Lys Lys Thr Glu Val Glu Ala Ser Thr Asn Gly  
 275 280 285

Thr Lys Lys Thr Glu Val Lys Lys Gly Val Ala Thr Ser Lys Pro Lys  
 290 295 300

Ala Ala Lys Pro Thr Ile Glu Ile Asp Asp Asp Asp Leu Pro Phe  
 305 310 315

<210> 40

<211> 797

<212> PRT

<213> Staphylococcus epidermidis

<400> 40

Leu Pro Gln Ala Lys Lys Arg Thr Ser Thr Lys Arg Lys Gly Asn Lys  
 1 5 10 15

Lys Thr Asn Lys Lys Lys Gln Asn Glu Thr Pro Leu Arg Tyr Ile Phe  
 20 25 30

Ser Ile Ile Val Val Ile Leu Ile Ile Leu Gly Ala Phe Gln Leu Gly  
 35 40 45

Ile Ile Gly Arg Met Ile Asp Ser Phe Phe Asn Tyr Leu Phe Gly Met  
 50 55 60

Ser Arg Tyr Leu Thr Tyr Ile Leu Val Leu Ile Ala Thr Ile Phe Ile  
 65 70 75 80

Thr Tyr Ser Lys Gln Ile Pro Arg Thr Arg Arg Ser Ile Gly Ala Ile  
 85 90 95

Val Leu Gln Leu Ala Leu Leu Phe Ile Ala Gln Leu Tyr Phe His Phe  
 100 105 110

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Ser His Asn Ile Thr Ser Gln Arg Glu Pro Val Leu Ser Phe Val Tyr  
 115 120 125

Lys Ala Tyr Glu Gln Thr His Phe Pro Asn Phe Gly Gly Gly Leu Ile  
 130 135 140

Gly Phe Tyr Leu Leu Lys Leu Phe Ile Pro Leu Ile Ser Ile Val Gly  
 145 150 155 160

Val Ile Ile Ile Thr Ile Leu Leu Leu Ala Ser Ser Phe Ile Leu Leu  
 165 170 175

Leu Asn Leu Arg His Arg Asp Val Thr Lys Ser Leu Phe Asp Asn Leu  
 180 185 190

Lys Ser Ser Ser Asn His Ala Ser Glu Ser Ile Lys Gln Lys Arg Glu  
 195 200 205

Gln Asn Lys Ile Lys Lys Glu Glu Lys Ala Gln Leu Lys Glu Ala Lys  
 210 215 220

Ile Glu Arg Lys Lys Gln Lys Lys Ser Arg Gln Asn Asn Asn Val Ile  
 225 230 235 240

Lys Asp Val Ser Asp Phe Pro Glu Ile Ser Gln Ser Asp Asp Ile Pro  
 245 250 255

Ile Tyr Gly His Asn Glu Gln Glu Asp Lys Arg Pro Asn Thr Ala Asn  
 260 265 270

Gln Arg Gln Lys Arg Val Leu Asp Asn Glu Gln Phe Gln Gln Ser Leu  
 275 280 285

Pro Ser Thr Lys Asn Gln Ser Ile Asn Asn Asn Gln Pro Ser Thr Thr  
 290 295 300

Ala Glu Asn Asn Gln Gln Gln Ser Gln Ala Glu Gly Ser Ile Ser Glu  
 305 310 315 320

Ala Gly Glu Glu Ala Asn Ile Glu Tyr Thr Val Pro Pro Leu Ser Leu  
 325 330 335

Leu Lys Gln Pro Thr Lys Gln Lys Thr Thr Ser Lys Ala Glu Val Gln  
 340 345 350

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Arg Lys Gly Gln Val Leu Glu Ser Thr Leu Lys Asn Phe Gly Val Asn  
 355 360 365

Ala Lys Val Thr Gln Ile Lys Ile Gly Pro Ala Val Thr Gln Tyr Glu  
 370 375 380

Ile Gln Pro Ala Gln Gly Val Lys Val Ser Lys Ile Val Asn Leu His  
 385 390 395 400

Asn Asp Ile Ala Leu Ala Leu Ala Ala Lys Asp Val Arg Ile Glu Ala  
 405 410 415

Pro Ile Pro Gly Arg Ser Ala Val Gly Ile Glu Val Pro Asn Asp Lys  
 420 425 430

Ile Ser Leu Val Thr Leu Lys Glu Val Leu Glu Asp Lys Phe Pro Ser  
 435 440 445

Lys Tyr Lys Leu Glu Val Gly Ile Gly Arg Asp Ile Ser Gly Asp Pro  
 450 455 460

Ile Ser Ile Gln Leu Asn Glu Met Pro His Leu Leu Val Ala Gly Ser  
 465 470 475 480

Thr Gly Ser Gly Lys Ser Val Cys Ile Asn Gly Ile Ile Thr Ser Ile  
 485 490 495

Leu Leu Asn Thr Lys Pro His Glu Val Lys Leu Met Leu Ile Asp Pro  
 500 505 510

Lys Met Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ile  
 515 520 525

Pro Val Val Thr Asn Pro His Lys Ala Ser Gln Ala Leu Glu Lys Ile  
 530 535 540

Val Ser Glu Met Glu Arg Arg Tyr Asp Leu Phe Gln His Ser Ser Thr  
 545 550 555 560

Arg Asn Ile Glu Gly Tyr Asn Gln Tyr Ile Arg Lys Gln Asn Glu Glu  
 565 570 575

Leu Asp Glu Lys Gln Pro Glu Leu Pro Tyr Ile Val Val Ile Val Asp  
 580 585 590

Glu Leu Ala Asp Leu Met Met Val Ala Gly Lys Glu Val Glu Asn Ala  
 595 600 605

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Ile Gln Arg Ile Thr Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile  
 610 615 620

Val Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Ile Ile Lys  
 625 630 635 640

Asn Asn Ile Pro Ser Arg Ile Ala Phe Ala Val Ser Ser Gln Thr Asp  
 645 650 655

Ser Arg Thr Ile Ile Gly Ala Gly Gly Ala Glu Lys Leu Leu Gly Lys  
 660 665 670

Gly Asp Met Leu Tyr Val Gly Asn Gly Glu Ser Thr Thr Thr Arg Ile  
 675 680 685

Gln Gly Ala Phe Leu Ser Asp Gln Glu Val Gln Asp Val Val Asn Tyr  
 690 695 700

Val Val Glu Gln Gln Lys Ala Asn Tyr Val Lys Glu Met Glu Pro Asp  
 705 710 715 720

Ala Pro Val Asp Lys Ser Glu Met Lys Ser Glu Asp Ala Leu Tyr Asp  
 725 730 735

Glu Ala Tyr Leu Phe Val Ile Glu Lys Gln Lys Ala Ser Thr Ser Leu  
 740 745 750

Leu Gln Arg Gln Phe Arg Ile Gly Tyr Asn Arg Ala Ser Arg Leu Met  
 755 760 765

Asp Asp Leu Glu Arg Asn Gln Val Ile Gly Pro Gln Lys Gly Ser Lys  
 770 775 780

Pro Arg Gln Ile Leu Val Asp Leu Glu Asn Asp Glu Val  
 785 790 795

<210> 41  
 <211> 429  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 41

Met Lys Thr His Gln Tyr Glu Leu Ile Asp Glu Lys Val Phe Glu His  
 1 5 10 15

Glu Phe Asp Asn Gly Leu Lys Leu Phe Ile Ile Pro Lys Pro Gly Phe

- 65 -

20

25

30

Gln Lys Thr Tyr Val Thr Tyr Thr Thr Gln Phe Gly Ser Leu Asp Asn  
 35 40 45

His Phe Lys Pro Ile Gly Ser Gln Gln Phe Val Lys Val Pro Asp Gly  
 50 55 60

Val Ala His Phe Leu Glu His Lys Leu Phe Glu Lys Glu Asp Glu Asp  
 65 70 75 80

Leu Phe Thr Ala Phe Ala Glu Glu Asn Ala Gln Ala Asn Ala Phe Thr  
 85 90 95

Ser Phe Asp Arg Thr Ser Tyr Leu Phe Ser Ala Thr Ser Asn Ile Glu  
 100 105 110

Ser Asn Ile Lys Arg Leu Leu Asn Met Val Glu Thr Pro Tyr Phe Thr  
 115 120 125

Glu Glu Thr Val Asn Lys Glu Lys Gly Ile Ile Ala Glu Glu Ile Lys  
 130 135 140

Met Tyr Gln Glu Gln Pro Gly Tyr Lys Leu Met Phe Asn Thr Leu Arg  
 145 150 155 160

Ala Met Tyr Ser Lys His Pro Ile Arg Val Asp Ile Ala Gly Ser Val  
 165 170 175

Glu Ser Ile Tyr Glu Ile Thr Lys Asp Asp Leu Tyr Leu Cys Tyr Glu  
 180 185 190

Thr Phe Tyr His Pro Ser Asn Met Val Leu Phe Val Val Gly Asp Val  
 195 200 205

Ser Pro Gln Ser Ile Ile Lys Leu Val Glu Lys His Glu Asn Gln Arg  
 210 215 220

Asn Lys Thr Tyr Gln Pro Arg Ile Glu Arg Ala Gln Ile Asp Glu Pro  
 225 230 235 240

Arg Glu Ile Asn Gln Arg Phe Val Ser Glu Lys Met Lys Leu Gln Ser  
 245 250 255

Pro Arg Leu Met Leu Gly Phe Lys Asn Glu Pro Leu Asp Glu Ser Ala  
 260 265 270

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Thr Lys Phe Val Gln Arg Asp Leu Glu Met Thr Phe Phe Tyr Glu Leu  
 275 280 285

Val Phe Gly Glu Glu Thr Glu Phe Tyr Gln Gln Leu Leu Asn Lys Asp  
 290 295 300

Leu Ile Asp Glu Thr Phe Gly Tyr Gln Phe Val Leu Glu Pro Ser Tyr  
 305 310 315 320

Ser Phe Ser Ile Ile Thr Ser Ala Thr Gln Gln Pro Asp Leu Phe Lys  
 325 330 335

Gln Leu Ile Met Asp Glu Leu Arg Lys Tyr Lys Gly Asn Leu Lys Asp  
 340 345 350

Gln Glu Ala Phe Asp Leu Leu Lys Lys Gln Phe Ile Gly Glu Phe Ile  
 355 360 365

Ser Ser Leu Asn Ser Pro Glu Tyr Ile Ala Asn Gln Tyr Ala Lys Leu  
 370 375 380

Tyr Phe Glu Gly Val Ser Val Phe Asp Met Leu Asp Ile Val Glu Asn  
 385 390 395 400

Ile Thr Leu Glu Ser Val Asn Glu Thr Ser Glu Leu Phe Leu Asn Phe  
 405 410 415

Asp Gln Leu Val Asp Ser Arg Leu Glu Met Glu Asn Arg  
 420 425

<210> 42  
 <211> 329  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 42

Met Thr Glu Gln Lys Asp Ile Lys Glu Thr Glu Tyr Arg Arg Gln Lys  
 1 5 10 15

Gly Thr Thr Ser Thr Pro Ser Arg Arg Arg Asn Lys Lys Arg Met Arg  
 20 25 30

Lys Leu Pro Phe Ile Ile Leu Val Ile Leu Ile Ile Leu Ile Ser Ile  
 35 40 45

Ile Val Tyr Ile Thr His Gln Tyr Asn Ser Gly Met Lys Tyr Ala Lys  
 50 55 60

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Glu His Ala Lys Asp Val Lys Val His Lys Phe Asn Gly Asn Met Lys  
65 70 75 80

Asn Asp Gly Lys Ile Ser Val Leu Val Leu Gly Ala Asp Lys Ala Gln  
85 90 95

Gly Gly Lys Ser Arg Thr Asp Ser Ile Met Ile Val Gln Tyr Asp Tyr  
100 105 110

Val His Lys Lys Met Lys Met Met Ser Val Met Arg Asp Ile Tyr Ala  
115 120 125

Asp Ile Pro Gly Tyr Asp Lys Tyr Lys Ile Asn Ala Ala Tyr Ser Leu  
130 135 140

Gly Gly Pro Glu Leu Leu Arg Lys Thr Leu Asn Lys Asn Leu Gly Val  
145 150 155 160

Asn Pro Glu Tyr Tyr Ala Val Val Asp Phe Thr Gly Phe Glu Lys Met  
165 170 175

Ile Asp Glu Leu Gln Pro Asn Gly Val Pro Ile Asp Val Glu Lys Asp  
180 185 190

Met Ser Glu Asn Ile Gly Val Ser Leu Lys Lys Gly His His Lys Leu  
195 200 205

Asn Gly Lys Glu Leu Leu Gly Tyr Ala Arg Phe Arg His Asp Pro Glu  
210 215 220

Gly Asp Phe Gly Arg Val Arg Arg Gln Gln Gln Val Met Gln Thr Leu  
225 230 235 240

Lys Gln Glu Leu Val Asn Phe Asn Thr Val Ala Lys Leu Pro Lys Val  
245 250 255

Ala Gly Ile Leu Arg Gly Tyr Val Asn Thr Asn Met Pro Asn Ser Ala  
260 265 270

Ile Phe Gln Thr Gly Ile Ser Phe Gly Ile Arg Gly Asp Lys Asp Val  
275 280 285

Gln Ser Leu Thr Val Pro Ile Lys Gly Ser Tyr Gln Asp Ile Asn Thr  
290 295 300

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Asn Asn Asp Gly Ser Ala Leu Gln Ile Asp Ser Glu Lys Asn Lys Gln  
 305 310 315 320

Ala Ile Lys Asn Phe Phe Glu Asp Asn  
 325

<210> 43  
 <211> 627  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 43

Met Glu Ala Tyr Lys Ile Glu His Leu Asn Lys Ser Tyr Ala Asp Lys  
 1 5 10 15

Glu Ile Phe Asn Asp Leu Asn Leu Ser Ile Ser Glu His Glu Arg Ile  
 20 25 30

Gly Leu Val Gly Ile Asn Gly Thr Gly Lys Ser Thr Leu Leu Lys Val  
 35 40 45

Ile Gly Gly Leu Asp Glu Asp Phe Thr Ala Asp Ile Thr His Pro Asn  
 50 55 60

Gln Tyr Arg Ile Arg Tyr Ser Ser Gln Lys Gln Asp Leu Asn Gly His  
 65 70 75 80

Met Thr Val Phe Glu Ala Val Leu Ser Ser Asp Thr Pro Thr Leu Arg  
 85 90 95

Ile Ile Lys Lys Tyr Glu Glu Ala Val Asn Arg Tyr Ala Leu Asp Gln  
 100 105 110

Ser Asp Ser Asn Phe Asn Lys Met Met Glu Ala Gln Glu Glu Met Asp  
 115 120 125

Gln Lys Asp Ala Trp Asp Tyr Asn Ala Glu Ile Lys Thr Ile Leu Ser  
 130 135 140

Lys Leu Gly Ile His Asp Thr Thr Lys Lys Ile Val Glu Leu Ser Gly  
 145 150 155 160

Gly Gln Gln Lys Arg Val Val Leu Ala Lys Thr Leu Ile Glu Gln Pro  
 165 170 175

Asp Leu Leu Leu Leu Asp Glu Pro Thr Asn His Leu Asp Phe Glu Ser  
 180 185 190



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Ile Arg Trp Leu Ile Asn Tyr Val Lys Gln Tyr Pro His Thr Val Leu  
 195 200 205

Phe Val Thr His Asp Arg Tyr Phe Leu Asn Glu Val Ser Thr Arg Ile  
 210 215 220

Ile Glu Leu Asp Arg Gly Lys Leu Lys Thr Tyr Pro Gly Asn Tyr Glu  
 225 230 235 240

Asp Tyr Ile Val Met Arg Ala Glu Asn Glu Leu Val Glu Gln Lys Gln  
 245 250 255

Gln Glu Lys Gln Lys Ala Leu Tyr Lys Gln Glu Leu Ala Trp Met Arg  
 260 265 270

Ala Gly Ala Lys Ala Arg Thr Thr Lys Gln Gln Ala Arg Ile Asn Arg  
 275 280 285

Phe Asn Gln Leu Glu Ser Asp Val Lys Thr Gln His Thr Gln Asp Lys  
 290 295 300

Gly Glu Leu Asn Leu Ala Tyr Ser Arg Leu Gly Lys Gln Val Tyr Glu  
 305 310 315 320

Leu Lys Asn Leu Ser Lys Ser Ile Asn Asn Lys Val Leu Phe Glu Asp  
 325 330 335

Val Thr Glu Ile Ile Gln Ser Gly Arg Arg Ile Gly Ile Val Gly Pro  
 340 345 350

Asn Gly Ala Gly Lys Thr Thr Leu Leu Asn Ile Leu Ser Asn Glu Asp  
 355 360 365

Gln Asp Tyr Glu Gly Glu Leu Lys Ile Gly Gln Thr Val Lys Val Ala  
 370 375 380

Tyr Phe Lys Gln Thr Glu Lys Thr Leu Asp Arg Asp Ile Arg Val Ile  
 385 390 395 400

Asp Tyr Leu Arg Glu Glu Ser Glu Met Ala Lys Glu Lys Asp Gly Thr  
 405 410 415

Ser Ile Ser Val Thr Gln Leu Leu Glu Arg Phe Leu Phe Pro Ser Ala  
 420 425 430

Thr His Gly Lys Lys Val Tyr Lys Leu Ser Gly Gly Glu Gln Lys Arg

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435                      440                      445  
 Leu Tyr Leu Leu Arg Leu Leu Val His Lys Pro Asn Val Leu Leu Leu  
     450                      455                      460  
 Asp Glu Pro Thr Asn Asp Leu Asp Thr Glu Thr Leu Thr Ile Leu Glu  
     465                      470                      475                      480  
 Asp Tyr Ile Asp Asp Phe Gly Gly Ser Val Ile Thr Val Ser His Asp  
                     485                      490                      495  
 Arg Tyr Phe Leu Asn Lys Val Val Gln Glu Tyr Trp Phe Ile His Asp  
                     500                      505                      510  
 Gly Lys Ile Glu Lys Ile Ile Gly Ser Phe Glu Asp Tyr Glu Ser Phe  
                     515                      520                      525  
 Lys Lys Glu His Glu Arg Gln Ala Met Leu Ser Lys Gln Thr Glu Gln  
                     530                      535                      540  
 Gln Asn Lys His Lys His Gln Pro Lys Lys Lys Thr Gly Leu Ser Tyr  
     545                      550                      555                      560  
 Lys Glu Lys Leu Glu Tyr Glu Thr Ile Met Thr Arg Ile Glu Met Thr  
                     565                      570                      575  
 Glu Thr Arg Leu Glu Asp Leu Glu Gln Glu Met Ile Asn Ala Ser Asp  
                     580                      585                      590  
 Asn Tyr Ala Arg Ile Lys Glu Leu Asn Glu Glu Lys Glu Gln Leu Glu  
                     595                      600                      605  
 Ala Thr Tyr Glu Ala Asp Ile Thr Arg Trp Ser Glu Leu Glu Glu Ile  
     610                      615                      620  
 Lys Glu Gln  
     625  
 <210> 44  
 <211> 270  
 <212> PRT  
 <213> Staphylococcus epidermidis  
 <400> 44  
 Met Lys Lys Leu Phe Gly Ile Ile Leu Val Leu Ala Leu Thr Ile Ala  
     1                      5                      10                      15

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Leu Ala Ala Cys Gly Gly Gly Lys Asp Lys Glu Lys Thr Ile Thr Val  
 20 25 30

Gly Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys Ala Lys Pro  
 35 40 45

Leu Leu Lys Lys Lys Gly Tyr Asp Leu Lys Ile Lys Pro Ile Asn Asp  
 50 55 60

Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile Asp Ala Asn  
 65 70 75 80

Phe Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Ser Lys Glu Lys Gly  
 85 90 95

Tyr Lys Ile Glu Ser Ala Gly Asn Val Glu Leu Glu Pro Met Ala Val  
 100 105 110

Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Asp Leu Pro Lys Gly Ala Thr  
 115 120 125

Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe Leu Lys Phe  
 130 135 140

Phe Val Asp Glu Gly Leu Ile Lys Leu Lys Lys Gly Val Lys Ile Glu  
 145 150 155 160

Asn Ala Lys Phe Asp Asp Ile Thr Glu Asn Lys Lys Asp Ile Lys Phe  
 165 170 175

Asn Asn Lys Gln Ser Ala Glu Tyr Leu Pro Lys Ile Tyr Gln Asn Gln  
 180 185 190

Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Tyr Ala Ile Asp Gln Lys  
 195 200 205

Leu Ser Pro Lys Lys Asp Ser Ile Ala Leu Glu Ser Pro Lys Asp Asn  
 210 215 220

Pro Tyr Ala Asn Leu Ile Ala Val Lys Lys Gly His Lys Asp Asp Lys  
 225 230 235 240

Asn Ile Lys Val Leu Met Glu Val Leu Gln Ser Lys Glu Ile Gln Asp  
 245 250 255

Tyr Ile Lys Asp Lys Tyr Asp Gly Ala Val Val Pro Ala Lys  
 260 265 270

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&lt;210&gt; 45

&lt;211&gt; 439

&lt;212&gt; PRT

&lt;213&gt; Staphylococcus epidermidis

&lt;400&gt; 45

Met	Glu	Leu	Thr	Ile	Tyr	His	Thr	Asn	Asp	Ile	His	Ser	His	Leu	Asn
1				5					10					15	

Glu	Tyr	Ala	Arg	Ile	Gln	Ala	Tyr	Met	Ala	Lys	His	Arg	Pro	Gln	Leu
		20						25					30		

Glu	His	Pro	Ser	Leu	Tyr	Ile	Asp	Ile	Gly	Asp	His	Val	Asp	Leu	Ser
		35					40					45			

Ala	Pro	Val	Thr	Glu	Ala	Thr	Val	Gly	His	Lys	Asn	Ile	Glu	Leu	Leu
	50					55					60				

Asn	Glu	Ala	His	Cys	Asp	Ile	Ala	Thr	Ile	Gly	Asn	Asn	Glu	Gly	Met
65					70					75					80

Thr	Ile	Ser	His	Asp	Ala	Leu	Gln	Asn	Leu	Tyr	Asn	Asp	Ala	Asp	Phe
			85						90					95	

Lys	Val	Ile	Cys	Thr	Asn	Val	Ile	Asp	Glu	Glu	Gly	His	Leu	Pro	His
			100					105					110		

His	Ile	Thr	Ser	Ser	Tyr	Ile	Lys	Glu	Ile	Lys	Gly	Thr	Arg	Ile	Leu
		115					120					125			

Phe	Val	Ala	Ala	Thr	Ala	Pro	Phe	Thr	Pro	Phe	Tyr	Arg	Ala	Leu	Asp
	130					135					140				

Trp	Ile	Val	Thr	Asp	Pro	Leu	Ala	Ala	Ile	Lys	Asp	Glu	Ile	Asn	Ala
145					150					155					160

His	Gln	Gly	Glu	Tyr	Asp	Leu	Leu	Met	Val	Met	Ser	His	Val	Gly	Ile
				165					170					175	

Phe	Phe	Asp	Glu	Lys	Leu	Cys	Gln	Glu	Ile	Pro	Glu	Ile	Asp	Val	Ile
		180						185					190		

Phe	Gly	Ser	His	Thr	His	His	His	Phe	Glu	His	Gly	Glu	Ile	Asn	Asn
		195					200					205			

Gly	Val	Leu	Met	Ala	Ala	Ala	Gly	Lys	Tyr	Gly	Tyr	Tyr	Leu	Gly	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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210	215	220
Val Asn Ile Thr Ile Glu Asn Gly Lys Ile Val Asp Lys Ile Ala Lys		
225	230	235 240
Ile His Pro Ile Glu Thr Leu Pro Leu Val Glu Thr His Phe Glu Glu		
	245	250 255
Glu Gly Arg Ala Leu Leu Ser Lys Pro Val Val Asn His His Val Asn		
	260	265 270
Leu Val Lys Arg Thr Asp Val Val Thr Arg Thr Ser Tyr Leu Leu Ala		
	275	280 285
Glu Ser Val Tyr Glu Phe Ser Arg Ala Asp Cys Ala Ile Val Asn Ala		
	290	295 300
Gly Leu Ile Val Asn Gly Ile Glu Ala Asp Lys Val Thr Glu Tyr Asp		
305	310	315 320
Ile His Arg Met Leu Pro His Pro Ile Asn Ile Val Arg Val Arg Leu		
	325	330 335
Thr Gly Lys Gln Leu Lys Gln Val Ile Gln Lys Ser Gln Lys Gln Glu		
	340	345 350
Tyr Met His Glu His Ala Gln Gly Leu Gly Phe Arg Gly Asp Ile Phe		
	355	360 365
Gly Gly Tyr Ile Leu Tyr Asn Leu Gly Phe Ile Glu Ser Glu Asp Arg		
	370	375 380
Tyr Phe Ile Gly Asp Glu Glu Ile Gln Asn Asp Lys Gln Tyr Thr Leu		
385	390	395 400
Gly Thr Val Asp Met Tyr Thr Phe Gly Arg Tyr Phe Pro Leu Leu Lys		
	405	410 415
Gly Leu Ser Thr Asp Tyr Ile Met Pro Glu Phe Leu Arg Asp Ile Phe		
	420	425 430
Lys Glu Lys Leu Leu Lys Leu		
	435	

<210> 46  
 <211> 203  
 <212> PRT

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&lt;213&gt; Staphylococcus epidermidis

&lt;400&gt; 46

Met Glu Lys Val Ile Tyr Leu Ala Gly His Ile Leu Asn Glu Ala Met  
 1 5 10 15

Val Asp Tyr Arg Glu Lys Gln His Asn Gln Val Glu Ala Ile Glu Gly  
 20 25 30

Val Lys Pro Tyr Ser Pro His Gln Asp Lys Ser Ile Asn Asp Lys Ser  
 35 40 45

Asn Ala Val Gln Glu Gly Leu Ala Glu Arg Ile Leu Lys Asn Asp Phe  
 50 55 60

Thr Ala Met Glu Lys Ser Asp Ile Tyr Val Leu Asp Val Leu Asn Glu  
 65 70 75 80

Gly Leu Gly Thr Ile Ser Glu Leu Gly Ile Ile Ile Gly Met Lys Lys  
 85 90 95

Gln Ala Gln Lys Thr Ile Asp Arg Leu Ser Val Leu Ser Glu Glu Ile  
 100 105 110

Lys His Asp Val Tyr Gly Asp Gln Thr Glu Ala Tyr Asp Leu Ile Gln  
 115 120 125

Asp Glu Ile Tyr Lys Gln Glu Lys Ile Leu Asn Lys Thr Val Leu Cys  
 130 135 140

Tyr Cys Ser Asp Ile Arg Gln Gly His Gly Lys Pro Tyr Thr Asp Pro  
 145 150 155 160

Asp Arg Ala Glu Phe Ser Thr Asn Gln Phe Val Tyr Gly Met Val Leu  
 165 170 175

Glu Ala Thr Asn Gly Glu Gly Phe Ile Thr Trp Asp Gln Val Leu His  
 180 185 190

Arg Leu Asp Leu Phe Gly Ser Gly Leu Ile Val  
 195 200

&lt;210&gt; 47

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Staphylococcus epidermidis

&lt;400&gt; 47

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Met Ser Lys Lys Phe Arg Val Glu Asp Lys Glu Thr Ile Ala Asp Cys  
 1 5 10 15

Leu Asp Arg Met Lys Lys Glu Gly Phe Met Pro Ile Arg Arg Ile Glu  
 20 25 30

Lys Pro Val Tyr Lys Glu Asn Lys Asp Gly Ser Ile Glu Ile Leu Lys  
 35 40 45

Gln Asp Ile Ile Phe Val Gly Ala Leu Ile Gln  
 50 55

<210> 48

<211> 3692

<212> PRT

<213> Staphylococcus epidermidis

<400> 48

Met Asn Leu Phe Arg Lys Gln Lys Phe Ser Ile Arg Lys Phe Asn Ile  
 1 5 10 15

Gly Ile Phe Ser Ala Leu Ile Ala Thr Val Ala Phe Leu Ala His Pro  
 20 25 30

Gly Gln Ala Thr Ala Ser Glu Leu Glu Pro Ser Gln Asn Asn Asp Thr  
 35 40 45

Thr Ala Gln Ser Asp Gly Gly Leu Glu Asn Thr Ser Gln Ser Asn Pro  
 50 55 60

Ile Ser Glu Glu Thr Thr Asn Thr Leu Ser Gly Gln Thr Val Pro Ser  
 65 70 75 80

Ser Thr Glu Asn Lys Gln Thr Gln Asn Val Pro Asn His Asn Ala Gln  
 85 90 95

Pro Ile Ala Ile Asn Thr Glu Glu Ala Glu Ser Ala Gln Thr Ala Ser  
 100 105 110

Tyr Thr Asn Ile Asn Glu Asn Asn Asp Thr Ser Asp Asp Gly Leu His  
 115 120 125

Val Asn Gln Pro Ala Lys His His Ile Glu Ala Gln Ser Glu Asp Val  
 130 135 140

Thr Asn His Thr Asn Ser Asn His Ser Asn Ser Ser Ile Pro Glu Asn  
 145 150 155 160

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Lys Ala Thr Thr Glu Ser Ser Ser Lys Pro Lys Lys Arg Gly Lys Arg  
 165 170 175

Ser Leu Asp Thr Asn Asn Gly Asn Asp Thr Thr Ser Thr Thr Gln Asn  
 180 185 190

Thr Asp Pro Asn Leu Ser Asn Thr Gly Pro Asn Gly Ile Asn Thr Val  
 195 200 205

Ile Thr Phe Asp Asp Leu Gly Ile Lys Thr Ser Thr Asn Arg Ser Arg  
 210 215 220

Pro Glu Val Lys Val Val Asp Ser Leu Asn Gly Phe Thr Met Val Asn  
 225 230 235 240

Gly Gly Lys Val Gly Leu Leu Asn Ser Val Leu Glu Arg Thr Ser Val  
 245 250 255

Phe Asp Ser Ala Asp Pro Lys Asn Tyr Gln Ala Ile Asp Asn Val Val  
 260 265 270

Ala Leu Gly Arg Ile Lys Gly Asn Asp Pro Asn Asp His Asp Gly Phe  
 275 280 285

Asn Gly Ile Glu Lys Glu Phe Ser Val Asn Pro Asn Ser Glu Ile Ile  
 290 295 300

Phe Ser Phe Asn Thr Met Thr Ala Lys Asn Arg Lys Gly Gly Thr Gln  
 305 310 315 320

Leu Val Leu Arg Asn Ala Glu Asn Asn Gln Glu Ile Ala Ser Thr Asp  
 325 330 335

Ile Gln Gly Gly Gly Val Tyr Arg Leu Phe Lys Leu Pro Asp Asn Val  
 340 345 350

His Arg Leu Lys Val Gln Phe Leu Pro Met Asn Glu Ile His Ser Asp  
 355 360 365

Phe Lys Arg Ile Gln Gln Leu His Asp Gly Tyr Arg Tyr Tyr Ser Phe  
 370 375 380

Ile Asp Thr Ile Gly Val Asn Ser Gly Ser His Leu Tyr Val Lys Ser  
 385 390 395 400



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Arg Gln Val Asn Lys Asn Val Lys Asn Gly Lys Glu Phe Glu Val Asn  
 405 410 415

Thr Arg Ile Glu Asn Asn Gly Asn Phe Ala Ala Ala Ile Gly Gln Asn  
 420 425 430

Glu Leu Thr Tyr Lys Val Thr Leu Pro Glu Asn Phe Glu Tyr Val Asp  
 435 440 445

Asn Ser Thr Glu Val Ser Phe Val Asn Gly Asn Val Pro Asn Ser Thr  
 450 455 460

Val Asn Pro Phe Ser Val Asn Phe Asp Arg Gln Asn His Thr Leu Thr  
 465 470 475 480

Phe Ser Ser Asn Gly Leu Asn Leu Gly Arg Ser Ala Gln Asp Val Ala  
 485 490 495

Arg Phe Leu Pro Asn Lys Ile Leu Asn Ile Arg Tyr Lys Leu Arg Pro  
 500 505 510

Val Asn Ile Ser Thr Pro Arg Glu Val Thr Phe Asn Glu Ala Ile Lys  
 515 520 525

Tyr Lys Thr Phe Ser Glu Tyr Tyr Ile Asn Thr Asn Asp Asn Thr Val  
 530 535 540

Thr Gly Gln Gln Thr Pro Phe Ser Ile Asn Val Ile Met Asn Lys Asp  
 545 550 555 560

Asp Leu Ser Glu Gln Val Asn Lys Asp Ile Ile Pro Ser Asn Tyr Thr  
 565 570 575

Leu Ala Ser Tyr Asn Lys Tyr Asn Lys Leu Lys Glu Arg Ala Gln Thr  
 580 585 590

Val Leu Asp Glu Glu Thr Asn Asn Thr Pro Phe Asn Gln Arg Tyr Ser  
 595 600 605

Gln Thr Gln Ile Asp Asp Leu Leu His Glu Leu Gln Thr Thr Leu Ile  
 610 615 620

Asn Arg Val Ser Ala Ser Arg Glu Ile Asn Asp Lys Ala Gln Glu Met  
 625 630 635 640

Thr Asp Ala Val Tyr Asp Ser Thr Glu Leu Thr Thr Glu Glu Lys Asp  
 645 650 655

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Thr Leu Val Asp Gln Ile Glu Asn His Lys Asn Glu Ile Ser Asn Asn  
                   660                                  665                                  670

Ile Asp Asp Glu Leu Thr Asp Asp Gly Val Glu Arg Val Lys Glu Ala  
                   675                                  680                                  685

Gly Leu His Thr Leu Glu Ser Asp Thr Pro His Pro Val Thr Lys Pro  
                   690                                  695                                  700

Asn Ala Arg Gln Val Val Asn Asn Arg Ala Asp Gln Gln Lys Thr Leu  
                   705                                  710                                  715                                  720

Ile Arg Asn Asn His Glu Ala Thr Thr Glu Glu Gln Asn Glu Ala Ile  
                                   725                                  730                                  735

Arg Gln Val Glu Ala His Ser Ser Asp Ala Ile Ala Lys Ile Gly Glu  
                   740                                  745                                  750

Ala Glu Thr Asp Thr Thr Val Asn Glu Ala Arg Asp Asn Gly Thr Lys  
                   755                                  760                                  765

Leu Ile Ala Thr Asp Val Pro Asn Pro Thr Lys Lys Ala Glu Ala Arg  
                   770                                  775                                  780

Ala Ala Val Thr Asn Ser Ala Asn Ser Lys Ile Lys Asp Ile Asn Asn  
                   785                                  790                                  795                                  800

Asn Thr Gln Ala Thr Leu Asp Glu Arg Asn Asp Ala Ile Ala Leu Val  
                                   805                                  810                                  815

Asn Arg Ser Lys Asp Glu Ala Ile Gln Asn Ile Asn Thr Ala Gln Gly  
                   820                                  825                                  830

Asn Asp Asp Val Thr Glu Ala Gln Asn Asn Gly Thr Asn Thr Ile Gln  
                   835                                  840                                  845

Gln Val Pro Leu Thr Pro Val Lys Arg Gln Asn Ala Ile Ala Thr Ile  
                   850                                  855                                  860

Asn Ala Lys Ala Asp Glu Gln Lys Arg Leu Ile Gln Ala Asn Asn Asn  
                   865                                  870                                  875                                  880

Ala Thr Thr Glu Glu Lys Ala Asp Ala Glu Arg Lys Val Asn Glu Ala  
                                   885                                  890                                  895

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Val Ile Thr Ala Asn Gln Asn Ile Thr Asn Ala Thr Thr Asn Arg Asp  
 900 905 910

Val Asp Gln Ala Gln Thr Thr Gly Ser Gly Ile Ile Ser Ala Ile Ser  
 915 920 925

Pro Ala Thr Lys Ile Lys Glu Asp Ala Arg Ala Ala Val Glu Ala Lys  
 930 935 940

Ala Ile Ala Gln Asn Gln Gln Ile Asn Ser Asn Asn Met Ala Thr Thr  
 945 950 955 960

Glu Glu Lys Glu Asp Ala Leu Asn Gln Val Glu Ala His Lys Gln Ala  
 965 970 975

Ala Ile Ala Thr Ile Asn Gln Ala Gln Ser Thr Gln Gln Val Ser Glu  
 980 985 990

Ala Lys Asn Asn Gly Ile Asn Thr Ile Asn Gln Asp Gln Pro Asn Ala  
 995 1000 1005

Val Lys Lys Asn Asn Thr Lys Ile Ile Leu Glu Gln Lys Gly Asn  
 1010 1015 1020

Glu Lys Lys Ser Ala Ile Ala Gln Thr Pro Asp Ala Thr Thr Glu  
 1025 1030 1035

Glu Lys Gln Glu Ala Val Ser Ala Val Ser Gln Ala Val Thr Asn  
 1040 1045 1050

Gly Ile Thr His Ile Asn Gln Ala Asn Ser Asn Asp Asp Val Asp  
 1055 1060 1065

Gln Glu Leu Ser Asn Ala Glu Gln Ile Ile Thr Gln Thr Asn Val  
 1070 1075 1080

Asn Val Gln Lys Lys Pro Gln Ala Arg Gln Ala Leu Ile Ala Lys  
 1085 1090 1095

Thr Asn Glu Arg Gln Ser Thr Ile Asn Thr Asp Asn Glu Gly Thr  
 1100 1105 1110

Ile Glu Glu Lys Gln Lys Ala Ile Gln Ser Leu Asn Asp Ala Lys  
 1115 1120 1125

Asn Leu Ala Asp Glu Gln Ile Thr Gln Ala Ala Ser Asn Gln Asn  
 1130 1135 1140

Val Asp Asn Ala Leu Asn Ile Gly Ile Ser Asn Ile Ser Lys Ile  
 1145 1150 1155  
 Gln Thr Asn Phe Thr Lys Lys Gln Gln Ala Arg Asp Gln Val Asn  
 1160 1165 1170  
 Gln Lys Phe Gln Glu Lys Glu Ala Glu Leu Asn Ser Thr Pro His  
 1175 1180 1185  
 Ala Thr Gln Asp Glu Lys Gln Asp Ala Leu Thr Arg Leu Thr Gln  
 1190 1195 1200  
 Ala Lys Glu Thr Ala Leu Asn Asp Ile Asn Gln Ala Gln Thr Asn  
 1205 1210 1215  
 Gln Asn Val Asp Thr Ala Leu Thr Ser Gly Ile Gln Asn Ile Gln  
 1220 1225 1230  
 Asn Thr Gln Val Asn Val Arg Lys Lys Gln Glu Ala Lys Thr Thr  
 1235 1240 1245  
 Ile Asn Asp Ile Val Gln Gln His Lys Gln Thr Ile Gln Asn Asn  
 1250 1255 1260  
 Asp Asp Ala Thr Thr Glu Glu Lys Glu Val Ala Asn Asn Leu Val  
 1265 1270 1275  
 Asn Ala Ser Gln Gln Asn Val Ile Ser Lys Ile Asp Asn Ala Thr  
 1280 1285 1290  
 Thr Asn Asn Gln Ile Asp Gly Ile Val Ser Asp Gly Arg Gln Ser  
 1295 1300 1305  
 Ile Asn Ala Ile Thr Pro Asp Thr Ser Ile Lys Arg Asn Ala Lys  
 1310 1315 1320  
 Asn Asp Ile Asp Ile Lys Ala Ala Asp Lys Lys Ile Lys Ile Gln  
 1325 1330 1335  
 Arg Ile Asn Asp Ala Thr Asp Glu Glu Ile Gln Glu Ala Asn Arg  
 1340 1345 1350  
 Lys Ile Glu Glu Ala Lys Ile Glu Ala Lys Asp Asn Ile Gln Arg  
 1355 1360 1365

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Asn Ser Thr Arg Asp Gln Val Asn Glu Ala Lys Thr Asn Gly Ile  
1370 1375 1380

Asn Lys Ile Glu Asn Ile Thr Pro Ala Thr Thr Val Lys Ser Glu  
1385 1390 1395

Ala Arg Gln Ala Val Gln Asn Lys Ala Asn Glu Gln Ile Asn His  
1400 1405 1410

Ile Gln Asn Thr Pro Asp Ala Thr Asn Glu Glu Lys Gln Glu Ala  
1415 1420 1425

Ile	Asn	Arg	Val	Ser	Ala	Glu	Leu	Ala	Arg	Val	Gln	Ala	Gln	Ile
	1430					1435					1440			

Asn Ala Glu His Thr Thr Gln Gly Val Lys Thr Ile Lys Asp Asp  
1445 1450 1455

Ala Ile Thr Ser Leu Ser Arg Ile Asn Ala Gln Val Val Glu Lys  
1460 1465 1470

Glu Ser Ala Arg Asn Ala Ile Glu Gln Lys Ala Thr Gln Gln Thr  
1475 1480 1485

Gln Phe Ile Asn Asn Asn Asp Asn Ala Thr Asp Glu Glu Lys Glu  
1490 1495 1500

Val Ala Asn Asn Leu Val Ile Ala Thr Lys Gln Lys Ser Leu Asp  
1505 1510 1515

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Asn Ile  Asn Ser  Leu Ser  Ser  Asn Asn Asp Val  Glu  Asn Ala Lys
1520                                1525          1530

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Val Ala Gly Ile Asn Glu Ile Ala Asn Val Leu Pro Ala Thr Ala  
1535 1540 1545

Val	Lys	Ser	Lys	Ala	Lys	Lys	Asp	Ile	Asp	Gln	Lys	Leu	Ala	Gln
	1550					1555					1560			

Gln Ile Asn Gln Ile Gln Thr His Gln Thr Ala Thr Thr Glu Glu  
1565 1570 1575

Lys Glu Ala Ala Ile Gln Leu Ala Asn Gln Lys Ser Asn Glu Ala  
1580 1585 1590

Arg Thr Ala Ile Gln Asn Glu His Ser Asn Asn Gly Val Ala Gln  
1595 1600 1605

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Ala Lys	Ser Asn Gly Ile His	Glu Ile Glu Leu Val	Met Pro Asp
1610	1615	1620	
Ala His	Lys Lys Ser Asp Ala	Lys Gln Ser Ile Asp	Asn Lys Tyr
1625	1630	1635	
Asn Glu	Gln Ser Asn Thr Ile	Asn Thr Thr Pro Asp	Ala Thr Asp
1640	1645	1650	
Glu Glu	Lys Gln Lys Ala Leu	Asp Lys Leu Lys Ile	Ala Lys Asp
1655	1660	1665	
Ala Gly	Tyr Asn Lys Val Asp	Gln Ala Gln Thr Asn	Gln Gln Val
1670	1675	1680	
Ser Asp	Ala Lys Thr Glu Ala	Ile Asp Thr Ile Thr	Asn Ile Gln
1685	1690	1695	
Ala Asn	Val Ala Lys Lys Pro	Ser Ala Arg Val Glu	Leu Asp Ser
1700	1705	1710	
Lys Phe	Glu Asp Leu Lys Arg	Gln Ile Asn Ala Thr	Pro Asn Ala
1715	1720	1725	
Thr Glu	Glu Glu Lys Gln Asp	Ala Ile Gln Arg Leu	Asn Gly Lys
1730	1735	1740	
Arg Asp	Glu Val Lys Asn Leu	Ile Asn Gln Asp Arg	Arg Asp Asn
1745	1750	1755	
Glu Val	Glu Gln His Lys Asn	Ile Gly Leu Gln Glu	Leu Glu Thr
1760	1765	1770	
Ile His	Ala Asn Pro Thr Arg	Lys Ser Asp Ala Leu	Gln Glu Leu
1775	1780	1785	
Gln Thr	Lys Phe Ile Ser Gln	Thr Glu Leu Ile Asn	Asn Asn Lys
1790	1795	1800	
Asp Ala	Thr Asn Glu Glu Lys	Asp Glu Ala Lys Arg	Leu Leu Glu
1805	1810	1815	
Ile Ser	Lys Asn Lys Thr Ile	Thr Asn Ile Asn Gln	Ala Gln Thr
1820	1825	1830	

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Asn	Asn	Gln	Val	Asp	Asn	Ala	Lys	Asp	Asn	Gly	Met	Asn	Glu	Ile
1835						1840					1845			
Ala	Thr	Ile	Ile	Pro	Ala	Thr	Thr	Ile	Lys	Thr	Asp	Ala	Lys	Thr
1850						1855					1860			
Ala	Ile	Asp	Lys	Lys	Ala	Glu	Gln	Gln	Val	Thr	Ile	Ile	Asn	Gly
1865						1870					1875			
Asn	Asn	Asp	Ala	Thr	Asp	Glu	Glu	Lys	Ala	Glu	Ala	Arg	Lys	Leu
1880						1885					1890			
Val	Glu	Lys	Ala	Lys	Ile	Glu	Ala	Lys	Ser	Asn	Ile	Thr	Asn	Ser
1895						1900					1905			
Asp	Thr	Glu	Arg	Glu	Val	Asn	Gly	Ala	Lys	Thr	Asn	Gly	Leu	Glu
1910						1915					1920			
Lys	Ile	Asn	Asn	Ile	Gln	Pro	Ser	Thr	Gln	Thr	Lys	Thr	Asn	Ala
1925						1930					1935			
Lys	Gln	Glu	Ile	Asn	Asp	Lys	Ala	Gln	Glu	Gln	Leu	Ile	Gln	Ile
1940						1945					1950			
Asn	Asn	Thr	Pro	Asp	Ala	Thr	Glu	Glu	Glu	Lys	Gln	Glu	Ala	Thr
1955						1960					1965			
Asn	Arg	Val	Asn	Ala	Gly	Leu	Ala	Gln	Ala	Ile	Gln	Asn	Ile	Asn
1970						1975					1980			
Asn	Ala	His	Ser	Thr	Gln	Glu	Val	Asn	Glu	Ser	Lys	Thr	Asn	Ser
1985						1990					1995			
Ile	Ala	Thr	Ile	Lys	Ser	Val	Gln	Pro	Asn	Val	Ile	Lys	Lys	Pro
2000						2005					2010			
Thr	Ala	Ile	Asn	Ser	Leu	Thr	Gln	Glu	Ala	Asn	Asn	Gln	Lys	Thr
2015						2020					2025			
Leu	Ile	Gly	Asn	Asp	Gly	Asn	Ala	Thr	Asp	Asp	Glu	Lys	Glu	Ala
2030						2035					2040			
Ala	Lys	Gln	Leu	Val	Thr	Gln	Lys	Leu	Asn	Glu	Gln	Ile	Gln	Lys
2045						2050					2055			
Ile	His	Glu	Ser	Thr	Gln	Asp	Asn	Gln	Val	Asp	Asn	Val	Lys	Ala
2060						2065					2070			

Gln Ala Ile Thr Ala Ile Lys Leu Ile Asn Ala Asn Ala His Lys  
 2075 2080 2085

Arg Gln Asp Ala Ile Asn Ile Leu Thr Asn Leu Ala Glu Ser Lys  
 2090 2095 2100

Lys Ser Asp Ile Arg Ala Asn Gln Asp Ala Thr Thr Glu Glu Lys  
 2105 2110 2115

Asn Thr Ala Ile Gln Ser Ile Asp Asp Thr Leu Ala Gln Ala Arg  
 2120 2125 2130

Asn Asn Ile Asn Gly Ala Asn Thr Asn Ala Leu Val Asp Glu Asn  
 2135 2140 2145

Leu Glu Asp Gly Lys Gln Lys Leu Gln Arg Ile Val Leu Ser Thr  
 2150 2155 2160

Gln Thr Lys Thr Gln Ala Lys Ala Asp Ile Ala Gln Ala Ile Gly  
 2165 2170 2175

Gln Gln Arg Ser Thr Ile Asp Gln Asn Gln Asn Ala Thr Thr Glu  
 2180 2185 2190

Glu Lys Gln Glu Ala Leu Glu Arg Leu Asn Gln Glu Thr Asn Gly  
 2195 2200 2205

Val Asn Asp Arg Ile Gln Ala Ala Leu Ala Asn Gln Asn Val Thr  
 2210 2215 2220

Asp Glu Lys Asn Asn Ile Leu Glu Thr Ile Arg Asn Val Glu Pro  
 2225 2230 2235

Ile Val Ile Val Lys Pro Lys Ala Asn Glu Ile Ile Arg Lys Lys  
 2240 2245 2250

Ala Ala Glu Gln Thr Thr Leu Ile Asn Gln Asn Gln Asp Ala Thr  
 2255 2260 2265

Leu Glu Glu Lys Gln Ile Ala Leu Gly Lys Leu Glu Glu Val Lys  
 2270 2275 2280

Asn Glu Ala Leu Asn Gln Val Ser Gln Ala His Ser Asn Asn Asp  
 2285 2290 2295



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Val Lys 2300	Ile Val Glu Asn Asn 2305	Gly Ile Ala Lys Ile 2310	Ser Glu Val
His Pro 2315	Glu Thr Ile Ile Lys 2320	Arg Asn Ala Lys Gln 2325	Glu Ile Glu
Gln Asp 2330	Ala Gln Ser Gln Ile 2335	Asp Thr Ile Asn Ala 2340	Asn Asn Lys
Ser Thr 2345	Asn Glu Glu Lys Ser 2350	Ala Ala Ile Asp Arg 2355	Val Asn Val
Ala Lys 2360	Ile Asp Ala Ile Asn 2365	Asn Ile Thr Asn Ala 2370	Thr Thr Thr
Gln Leu 2375	Val Asn Asp Ala Lys 2380	Asn Ser Gly Asn Thr 2385	Ser Ile Ser
Gln Ile 2390	Leu Pro Ser Thr Ala 2395	Val Lys Thr Asn Ala 2400	Leu Ala Ala
Leu Ala 2405	Ser Glu Ala Lys Asn 2410	Lys Asn Ala Ile Ile 2415	Asp Gln Thr
Pro Asn 2420	Ala Thr Ala Glu Glu 2425	Lys Glu Glu Ala Asn 2430	Asn Lys Val
Asp Arg 2435	Leu Gln Glu Glu Ala 2440	Asp Ala Asn Ile Leu 2445	Lys Ala His
Thr Thr 2450	Asp Glu Val Asn Asn 2455	Ile Lys Asn Gln Ala 2460	Val Gln Asn
Ile Asn 2465	Ala Val Gln Val Glu 2470	Val Ile Lys Lys Gln 2475	Asn Ala Lys
Asn Gln 2480	Leu Asn Gln Phe Ile 2485	Asp Asn Gln Lys Lys 2490	Ile Ile Glu
Asn Thr 2495	Pro Asp Ala Thr Leu 2500	Glu Glu Lys Ala Glu 2505	Ala Asn Arg
Leu Leu 2510	Gln Asn Val Leu Thr 2515	Ser Thr Ser Asp Glu 2520	Ile Ala Asn
Val Asp 2525	His Asn Asn Glu Val 2530	Asp Gln Ala Leu Asp 2535	Lys Ala Arg

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Pro Lys Ile Glu Ala Ile Val Pro Gln Val Ser Lys Lys Arg Asp  
 2540 2545 2550  
 ...

Ala Leu Asn Ala Ile Gln Glu Ala Phe Asn Ser Gln Thr Gln Glu  
 2555 2560 2565

Ile Gln Glu Asn Gln Glu Ala Thr Asn Glu Glu Lys Thr Glu Ala  
 2570 2575 2580

Leu Asn Lys Ile Asn Gln Leu Leu Asn Gln Ala Lys Val Asn Ile  
 2585 2590 2595

Asp Gln Ala Gln Ser Asn Lys Asp Val Asp Ser Ala Lys Thr Arg  
 2600 2605 2610

Ser Ile Gln Asp Ile Glu Gln Ile Gln Pro His Pro Gln Thr Lys  
 2615 2620 2625

Ala Thr Gly Arg His Arg Leu Asn Glu Lys Ala Asn Gln Gln Gln  
 2630 2635 2640

Ser Thr Ile Ala Thr His Pro Asn Ser Thr Ile Glu Glu Arg Gln  
 2645 2650 2655

Glu Ala Ser Ala Lys Leu Gln Glu Val Leu Lys Lys Ala Ile Ala  
 2660 2665 2670

Lys Ile Asp Lys Gly Gln Thr Asn Asp Asp Val Glu Lys Thr Val  
 2675 2680 2685

Val Asn Gly Ile Ala Glu Ile Glu Asn Ile Leu Pro Ala Thr Thr  
 2690 2695 2700

Val Lys Asp Lys Ala Lys Ala Asp Val Asn Ala Glu Lys Glu Glu  
 2705 2710 2715

Lys Asn Leu Gln Ile Asn Ser Asn Asp Glu Ala Thr Thr Glu Glu  
 2720 2725 2730

Lys Leu Val Ala Ser Asp Asn Leu Asn His Val Val Glu Thr Thr  
 2735 2740 2745

Asn Gln Ala Ile Glu Asp Ala Pro Asp Thr Asn Gln Val Asn Val  
 2750 2755 2760

Glu	Lys	Asn	Lys	Gly	Ile	Gly	Thr	Ile	Arg	Asp	Ile	Gln	Pro	Leu
2765						2770					2775			
Val	Val	Lys	Lys	Pro	Thr	Ala	Lys	Ser	Lys	Ile	Glu	Ser	Ala	Val
2780						2785					2790			
Glu	Lys	Lys	Lys	Thr	Glu	Ile	Asn	Gln	Thr	Gln	Asn	Ala	Thr	His
2795						2800					2805			
Asp	Glu	Val	Arg	Glu	Gly	Leu	Asn	Gln	Leu	Asn	Gln	Ile	His	Glu
2810						2815					2820			
Lys	Ala	Lys	Asn	Asp	Val	Asn	Gln	Ser	Gln	Thr	Asn	Gln	Gln	Val
2825						2830					2835			
Glu	Asn	Ala	Glu	Gln	Asn	Ser	Leu	Asp	Gln	Ile	Asn	Asn	Phe	Arg
2840						2845					2850			
Pro	Asp	Phe	Ser	Lys	Lys	Arg	Asn	Ala	Val	Ala	Glu	Ile	Val	Lys
2855						2860					2865			
Ala	Gln	Gln	Asn	Lys	Ile	Asp	Glu	Ile	Glu	Gln	Glu	Phe	Ser	Ala
2870						2875					2880			
Thr	Gln	Glu	Glu	Lys	Asp	Asn	Ala	Leu	Gln	His	Leu	Asp	Glu	Gln
2885						2890					2895			
Val	Lys	Glu	Ile	Ile	Asn	Ser	Ile	Asn	Gln	Ala	Asn	Thr	Asp	Asn
2900						2905					2910			
Glu	Val	Asp	Asn	Ala	Lys	Thr	Ser	Gly	Leu	Asn	Asn	Ile	Thr	Glu
2915						2920					2925			
Tyr	Arg	Pro	Glu	Tyr	Asn	Lys	Lys	Lys	Asn	Ala	Ile	Leu	Lys	Leu
2930						2935					2940			
Tyr	Asp	Val	Ser	Asp	Thr	Gln	Glu	Ala	Ile	Ile	Asn	Gly	Tyr	Pro
2945						2950					2955			
Asp	Ala	Thr	Glu	Asp	Glu	Leu	Gln	Glu	Ala	Asn	Ser	Lys	Leu	Asn
2960						2965					2970			
Lys	Ile	Leu	Leu	Asp	Ala	Lys	Lys	Gln	Ile	Gly	Leu	Ala	His	Thr
2975						2980					2985			
Asn	Asn	Glu	Val	Asp	Asp	Ile	Tyr	Asn	Glu	Val	Ser	Gln	Lys	Met
2990						2995					3000			

Lys Thr Ile Leu Pro Arg Val Asp Thr Lys Ala Val Ala Arg Ser  
3005 3010 3015

Val Leu Asn Ala Leu Ala Lys Gln Leu Ile Lys Thr Phe Glu Asn  
3020 3025 3030

Thr Ala Asp Val Thr His Glu Glu Arg Asn Asp Ala Ile Asn His  
3035 3040 3045

Val Lys Glu Gln Leu Ser Leu Val Phe Asn Ala Ile Glu Lys Asp  
3050 3055 3060

Arg Lys Asp Ile Gln Val Ala Gln Asp Glu Leu Phe Gly Leu Asn  
3065 3070 3075

Glu Leu Asn Ser Ile Phe Ile Asn Ile Thr Gln Lys Pro Thr Ala  
3080 3085 3090

Arg Lys Ala Ile Ser Gly Met Ala Ser Gln Leu Asn Asn Ser Ile  
3095 3100 3105

Asn Asn Thr Pro Tyr Ala Thr Glu Glu Glu Arg Gln Ile Ala Leu  
3110 3115 3120

Asn Lys Val Lys Ala Ile Val Asp Asp Ala Asn Glu Lys Ile Arg  
3125 3130 3135

Glu Ala Asn Thr Asp Ser Glu Val Leu Gly Thr Lys Ser Asn Ala  
3140 3145 3150

Ile Thr Leu Leu Gln Ala Ile Ser Ala Asp Val Gln Val Lys Pro  
3155 3160 3165

Gln Ala Phe Glu Glu Ile Asn Ala Gln Ala Glu Ile Gln Arg Glu  
3170 3175 3180

Arg Ile Asn Gly Asn Ser Asp Ala Thr Arg Glu Glu Lys Glu Glu  
3185 3190 3195

Ala Leu Lys Gln Val Asp Thr Leu Val Asn His Ser Phe Ile Thr  
3200 3205 3210

Ile Asn Asn Val Asn Lys Asn Gln Glu Val Tyr Asp Thr Lys Asp  
3215 3220 3225

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Lys Thr Ile Glu Ala Ile His Lys Ile Lys Pro Ile Ser Thr Ile  
 3230 3235 3240

Lys Pro Gln Ala Leu Asn Glu Ile Thr Ile Gln Leu Asp Thr Gln  
 3245 3250 3255

Arg Asp Leu Ile Lys Asn Asn Lys Glu Ser Thr Val Glu Glu Lys  
 3260 3265 3270

Ala Ser Ala Ile Asp Lys Leu Ile Lys Thr Ala Ala Arg Ile Ala  
 3275 3280 3285

Glu Ser Ile Asp Lys Ala Gln Thr Asn Glu Glu Val Lys Asn Ile  
 3290 3295 3300

Lys Lys Gln Ser Ile Asp Glu Ile Ser Lys Ile Leu Pro Val Ile  
 3305 3310 3315

Glu Ile Lys Ser Ala Ala Arg Asn Glu Ile His Gln Lys Ala Glu  
 3320 3325 3330

Val Ile Arg Gly Leu Ile Asn Asp Asn Glu Glu Ala Thr Lys Glu  
 3335 3340 3345

Glu Lys Asp Ile Ala Leu Asn Gln Leu Asp Thr Thr Leu Thr Gln  
 3350 3355 3360

Ala Asn Val Ser Ile Asp Gln Ala Leu Thr Asn Glu Ala Val Asn  
 3365 3370 3375

Arg Ala Lys Glu Ile Ala Asn Ser Glu Ile Asn Lys Ile Ser Val  
 3380 3385 3390

Ile Ala Ile Lys Lys Pro Glu Ala Ile Ala Glu Ile Gln Glu Leu  
 3395 3400 3405

Ala Asp Lys Lys Leu Asn Lys Phe Lys Gln Ser Gln Glu Ala Thr  
 3410 3415 3420

Ile Glu Glu Lys Gln Ser Ala Ile Asn Glu Leu Glu Gln Ala Leu  
 3425 3430 3435

Lys Ser Ala Ile Asn His Ile His Gln Ser Gln Asn Asn Glu Ser  
 3440 3445 3450

Val Ser Ala Ala Leu Lys Glu Ser Ile Ser Leu Ile Asp Ser Ile  
 3455 3460 3465

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Glu Ile Gln Ala His Lys Lys Leu Glu Ala Lys Ala Tyr Ile Asp  
 3470 3475 3480

Gly Tyr Ser Asp Asp Lys Ile Asn Asp Ile Ser Ser Arg Ala Thr  
 3485 3490 3495

Asn Glu Glu Lys Gln Ile Phe Val Ser Lys Leu Lys Ala Leu Ile  
 3500 3505 3510

Asn Arg Thr His Lys Gln Ile Asp Glu Ala Glu Thr Phe Val Ser  
 3515 3520 3525

Val Glu Thr Ile Val Arg Asn Phe Lys Val Glu Ala Asp Lys Leu  
 3530 3535 3540

Asn Ser Ile Val Arg Lys Lys Ala Lys Ala Ser Lys Glu Ile Glu  
 3545 3550 3555

Leu Glu Ala Asp His Val Lys Gln Met Ile Asn Ala Asn Leu Ser  
 3560 3565 3570

Ala Ser Thr Arg Val Lys Gln Asn Ala Arg Thr Leu Ile Asn Glu  
 3575 3580 3585

Ile Val Ser Asn Ala Leu Ser Gln Leu Asn Lys Val Thr Thr Asn  
 3590 3595 3600

Lys Glu Val Asp Glu Ile Val Asn Glu Thr Ile Glu Lys Leu Lys  
 3605 3610 3615

Ser Ile Gln Ile Arg Glu Asp Lys Ile Leu Ser Ser Gln Arg Ser  
 3620 3625 3630

Ser Thr Ser Met Thr Glu Lys Ser Asn Gln Cys Tyr Ser Ser Glu  
 3635 3640 3645

Asn Asn Thr Ile Lys Ser Leu Pro Glu Ala Gly Asn Ala Asp Lys  
 3650 3655 3660

Ser Leu Pro Leu Ala Gly Val Thr Leu Ile Ser Gly Leu Ala Ile  
 3665 3670 3675

Met Ser Ser Arg Lys Lys Lys Lys Asp Lys Lys Val Asn Asp  
 3680 3685 3690

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<210> 49  
 <211> 439  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 49

Leu Asp Ile Lys Met Pro Lys Leu Gly Glu Ser Val His Glu Gly Thr  
 1 5 10 15

Ile Glu Gln Trp Leu Val Ser Val Gly Asp His Val Asp Glu Tyr Glu  
 20 25 30

Pro Leu Cys Glu Val Ile Thr Asp Lys Val Thr Ala Glu Val Pro Ser  
 35 40 45

Thr Ile Ser Gly Thr Ile Thr Glu Leu Val Val Glu Glu Gly Gln Thr  
 50 55 60

Val Asn Ile Asn Thr Val Ile Cys Lys Ile Asp Ser Glu Asn Gly Gln  
 65 70 75 80

Asn Gln Thr Glu Ser Ala Asn Glu Phe Lys Glu Glu Gln Asn Gln His  
 85 90 95

Ser Gln Ser Asn Ile Asn Val Ser Gln Phe Glu Asn Asn Pro Lys Thr  
 100 105 110

His Glu Ser Glu Val His Thr Ala Ser Ser Arg Ala Asn Asn Asn Gly  
 115 120 125

Arg Phe Ser Pro Val Val Phe Lys Leu Ala Ser Glu His Asp Ile Asp  
 130 135 140

Leu Thr Gln Val Lys Gly Thr Gly Phe Glu Gly Arg Val Thr Lys Lys  
 145 150 155 160

Asp Ile Gln Asn Ile Ile Asn Asn Pro Asn Asp Gln Glu Lys Glu Lys  
 165 170 175

Glu Phe Lys Gln Thr Asp Lys Lys Asp His Ser Thr Asn His Cys Asp  
 180 185 190

Phe Leu His Gln Ser Ser Thr Lys Asn Glu His Ser Pro Leu Ser Asn  
 195 200 205

Glu Arg Val Val Pro Val Lys Gly Ile Arg Lys Ala Ile Ala Gln Asn  
 210 215 220

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Met Val Thr Ser Val Ser Glu Ile Pro His Gly Trp Met Met Val Glu  
225 230 235 240

Ala Asp Ala Thr Asn Leu Val Gln Thr Arg Asn Tyr His Lys Ala Gln  
245 250 255

Phe Lys Gln Asn Glu Gly Tyr Asn Leu Thr Phe Phe Ala Phe Phe Val  
260 265 270

Lys Ala Val Ala Glu Ala Leu Lys Val Asn Pro Leu Leu Asn Ser Thr  
275 280 285

Trp Gln Gly Asp Glu Ile Val Ile His Lys Asp Ile Asn Ile Ser Ile  
290 295 300

Ala Val Ala Asp Asp Asp Lys Leu Tyr Val Pro Val Ile Lys Asn Ala  
305 310 315 320

Asp Glu Lys Ser Ile Lys Gly Ile Ala Arg Glu Ile Asn Asp Leu Ala  
325 330 335

Thr Lys Ala Arg Leu Gly Lys Leu Ala Gln Ser Asp Met Gln Asn Gly  
340 345 350

Thr Phe Thr Val Asn Asn Thr Gly Ser Phe Gly Ser Val Ser Ser Met  
355 360 365

Gly Ile Ile Asn His Pro Gln Ala Ala Ile Leu Gln Val Glu Ser Val  
370 375 380

Val Lys Lys Pro Val Val Ile Asp Asp Met Ile Ala Ile Arg Asn Met  
385 390 395 400

Val Asn Leu Cys Ile Ser Ile Asp His Arg Ile Leu Asp Gly Val Gln  
405 410 415

Thr Gly Lys Phe Met Asn Leu Val Lys Lys Lys Ile Glu Gln Tyr Ser  
420 425 430

Ile Glu Asn Thr Ser Ile Tyr  
435

<210> 50

<211> 295

<212> PRT

<213> Staphylococcus epidermidis



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&lt;400&gt; 50

Met Asn Thr Ile Ile Glu Glu Tyr Leu Asn Phe Ile Gln Ile Glu Lys  
 1 5 10 15

Gly Leu Ser Asn Asn Thr Ile Gly Ala Tyr Arg Arg Asp Leu Lys Lys  
 20 25 30

Tyr Lys Asp Tyr Leu Glu Asp Asn Lys Ile Ser His Ile Asp Phe Ile  
 35 40 45

Asp Arg Gln Ile Ile Gln Glu Cys Leu Gly His Leu Ile Asp Met Gly  
 50 55 60

Gln Ser Ser Lys Ser Leu Ala Arg Phe Ile Ser Thr Ile Arg Ser Phe  
 65 70 75 80

His Gln Phe Ala Leu Arg Glu Lys Tyr Ala Ala Lys Asp Pro Thr Val  
 85 90 95

Leu Ile Glu Thr Pro Lys Tyr Glu Lys Lys Leu Pro Asp Val Leu Glu  
 100 105 110

Ile Asp Glu Val Ile Ala Leu Leu Glu Thr Pro Asp Leu Thr Lys Asn  
 115 120 125

Asn Gly Tyr Arg Asp Arg Thr Met Leu Glu Leu Leu Tyr Ala Thr Gly  
 130 135 140

Met Arg Val Thr Glu Ile Ile Gln Leu Asp Val Glu Asp Val Asn Leu  
 145 150 155 160

Met Met Gly Phe Val Arg Val Phe Gly Lys Gly Asn Lys Glu Arg Ile  
 165 170 175

Val Pro Leu Gly Asp Thr Val Ile Glu Tyr Leu Thr Thr Tyr Ile Glu  
 180 185 190

Thr Val Arg Pro Gln Leu Leu Lys Gln Thr Thr Thr Gln Ala Leu Phe  
 195 200 205

Leu Asn Met His Gly Lys Ser Leu Ser Arg Gln Gly Ile Trp Lys Ile  
 210 215 220

Ile Lys Gln Tyr Gly Leu Lys Ala Asn Ile Asn Lys Thr Leu Thr Pro  
 225 230 235 240

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His Thr Leu Arg His Ser Phe Ala Thr His Leu Leu Glu Asn Gly Ala  
                   245                  250                  255

Asp Leu Arg Ala Val Gln Glu Met Leu Gly His Ser Asp Ile Ser Thr  
                   260                  265                  270

Thr Gln Leu Tyr Thr His Val Ser Lys Ser Gln Ile Arg Lys Met Tyr  
                   275                  280                  285

Thr Gln Phe His Pro Arg Ala  
                   290                  295

<210> 51  
 <211> 800  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 51

Met Ser Leu Val Tyr Leu Met Ala Thr Asn Leu Leu Val Met Leu Ile  
 1                  5                  10                  15

Val Leu Phe Thr Leu Ser His Arg Gln Leu Arg Lys Val Ala Gly Tyr  
                   20                  25                  30

Val Ala Leu Ile Ala Pro Ile Val Thr Ser Thr Tyr Phe Ile Met Lys  
                   35                  40                  45

Ile Pro Asp Val Ile Arg Asn Lys Phe Ile Ala Val Arg Leu Pro Trp  
                   50                  55                  60

Met Pro Ser Ile Asp Ile Asn Leu Asp Leu Arg Leu Asp Gly Leu Ser  
 65                  70                  75                  80

Leu Met Phe Gly Leu Ile Ile Ser Leu Ile Gly Val Gly Val Phe Phe  
                   85                  90                  95

Tyr Ala Thr Gln Tyr Leu Ser His Ser Thr Asp Asn Leu Pro Arg Phe  
                   100                  105                  110

Phe Ile Tyr Leu Leu Leu Phe Met Phe Ser Met Ile Gly Ile Val Ile  
                   115                  120                  125

Ala Asn Asn Thr Ile Leu Met Tyr Val Phe Trp Glu Leu Thr Ser Ile  
                   130                  135                  140

Ser Ser Phe Leu Leu Ile Ser Tyr Trp Tyr Asn Asn Gly Glu Ser Gln  
 145                  150                  155                  160

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Leu Gly Ala Ile Gln Ser Phe Met Ile Thr Val Phe Gly Gly Leu Ala  
 165 170 175

Leu Leu Thr Gly Phe Ile Ile Leu Tyr Ile Ile Thr Gly Thr Asn Thr  
 180 185 190

Ile Thr Asp Ile Leu Asn Gln Arg Asn Ala Ile Ser Arg His Pro Leu  
 195 200 205

Phe Ile Pro Met Ile Leu Met Leu Leu Leu Gly Ala Phe Thr Lys Ser  
 210 215 220

Ala Gln Phe Pro Phe His Ile Trp Leu Pro Lys Ala Met Ala Ala Pro  
 225 230 235 240

Thr Pro Val Ser Ala Tyr Leu His Ser Ala Thr Met Val Lys Ala Gly  
 245 250 255

Ile Phe Leu Leu Phe Arg Phe Thr Pro Leu Leu Gly Leu Ser Asn Val  
 260 265 270

Tyr Ile Tyr Thr Val Thr Phe Val Gly Leu Ile Thr Met Leu Phe Gly  
 275 280 285

Ser Leu Thr Ala Leu Arg Gln Tyr Asp Leu Lys Gly Ile Leu Ala Tyr  
 290 295 300

Ser Thr Ile Ser Gln Leu Gly Met Ile Met Thr Met Val Gly Leu Gly  
 305 310 315 320

Gly Gly Tyr Ala Gln His Thr Ser Asp Glu Leu Ser Lys Phe Tyr Ile  
 325 330 335

Leu Val Leu Phe Ala Gly Leu Phe His Leu Met Asn His Ala Val Phe  
 340 345 350

Lys Cys Ala Leu Phe Met Gly Val Gly Ile Ile Asp His Glu Ser Gly  
 355 360 365

Thr Arg Asp Ile Arg Leu Leu Asn Gly Met Arg Lys Val Phe Pro Lys  
 370 375 380

Met His Ile Val Met Leu Leu Ala Ala Leu Ser Met Ala Gly Val Pro  
 385 390 395 400

Phe Leu Asn Gly Phe Leu Ser Lys Glu Met Phe Leu Asp Ser Leu Thr

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405

410

415

Lys Ala Asn Glu Leu Asp Gln Tyr Gly Phe Val Leu Thr Phe Val Ile  
 420 425 430

Ile Ser Ile Gly Val Ile Ala Ser Ile Leu Thr Phe Thr Tyr Ala Leu  
 435 440 445

Tyr Met Ile Lys Glu Thr Phe Trp Gly Asn Tyr Asn Ile Glu Lys Phe  
 450 455 460

Lys Arg Lys Gln Ile His Glu Pro Trp Leu Phe Ser Leu Pro Ala Val  
 465 470 475 480

Ile Leu Met Leu Leu Ile Pro Val Ile Phe Phe Val Pro Asn Val Phe  
 485 490 495

Gly Asn Phe Val Ile Leu Pro Ala Thr Arg Ser Val Ser Gly Ile Gly  
 500 505 510

Ala Glu Val Asp Ala Phe Val Pro His Ile Ser Gln Trp His Gly Val  
 515 520 525

Asn Leu Pro Leu Ile Leu Ser Ile Val Val Ile Ile Ile Gly Leu Ile  
 530 535 540

Leu Ala Leu Val Val Asn Trp Lys Glu Val Thr His Gln Ile Ile Lys  
 545 550 555 560

Ser Ala Ser Ile Thr Asp Gly Tyr Arg Lys Ile Tyr Arg Glu Phe Glu  
 565 570 575

Leu Tyr Ser Ala Arg Gly Ile Arg Ala Leu Met Asn Asn Lys Leu Asn  
 580 585 590

Tyr Tyr Ile Met Ile Thr Leu Phe Ile Phe Val Ala Ile Val Val Tyr  
 595 600 605

Gly Tyr Leu Thr Val Gly Phe Pro His Val His Gln Leu His Ile Ser  
 610 615 620

Ser Phe Gly Pro Leu Glu Val Ile Leu Ser Val Val Thr Leu Ile Ile  
 625 630 635 640

Gly Ile Ser Leu Ile Phe Ile Arg Gln Arg Leu Thr Met Val Val Leu  
 645 650 655

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Asn Gly Met Ile Gly Phe Ala Val Thr Leu Tyr Phe Ile Ala Met Lys  
660 665 670

Ala Pro Asp Leu Ala Leu Thr Gln Leu Val Val Glu Thr Ile Thr Thr  
675 680 685

Ile Leu Phe Ile Val Ser Phe Ser Arg Leu Pro Asn Ile Pro Arg Val  
690 695 700

Lys Ala Asn Leu Lys Lys Glu Thr Phe Lys Ile Ile Val Ser Leu Val  
705 710 715 720

Met Ala Leu Thr Val Val Ser Leu Ile Phe Val Ala Gln Gln Ala Asp  
725 730 735

Gly Met Pro Ser Ile Ala Lys Phe Tyr Glu Asp Ala Tyr Glu Leu Thr  
740 745 750

Gly Gly Lys Asn Ile Val Asn Ala Ile Leu Gly Asp Phe Arg Ala Leu  
755 760 765

Asp Thr Met Phe Glu Gly Leu Val Leu Ile Ile Ala Gly Leu Gly Ile  
770 775 780

Tyr Thr Leu Leu Asn Tyr Lys Asp Arg Arg Gly Gln Asp Glu Arg Glu  
785 790 795 800

&lt;210&gt; 52

<211> 892

<212> PRT

<213> Staphylococcus epidermidis

<400> 52

Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Thr Val  
1                  5                       10                       15

Gln Asp Val Lys Asp Ser Asn Met Asp Asp Glu Leu Ser Asp Ser Asn  
20 25 30

Asp Gln Ser Ser Asn Glu Glu Lys Asn Asp Val Ile Asn Asn Ser Gln  
35 40 45

Ser Ile Asn Thr Asp Asp Asp Asn Gln Ile Lys Lys Glu Glu Thr Asn  
50 55 60

Ser Asn Asp Ala Ile Glu Asn Arg Ser Lys Asp Ile Thr Gln Ser Thr  
65 70 75 80

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Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln  
 85 90 95

Asp Asn Thr Gln Leu Lys Glu Glu Val Val Lys Glu Pro Ser Ser Val  
 100 105 110

Glu Ser Ser Asn Ser Ser Met Asp Thr Ala Gln Gln Pro Ser His Thr  
 115 120 125

Thr Ile Asn Ser Glu Ala Ser Ile Gln Thr Ser Asp Asn Glu Glu Asn  
 130 135 140

Ser Arg Val Ser Asp Phe Ala Asn Ser Lys Ile Ile Glu Ser Asn Thr  
 145 150 155 160

Glu Ser Asn Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys Val Arg  
 165 170 175

Glu Asp Ser Ile Thr Ser Gln Pro Ser Ser Tyr Lys Asn Ile Asp Glu  
 180 185 190

Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn Glu Tyr  
 195 200 205

Glu Asn Lys Val Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro Ser Ser  
 210 215 220

Lys Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser Asn Val  
 225 230 235 240

Asn His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly Tyr Asp  
 245 250 255

Asp Ser Asp Gly Ile Ile Lys Ala His Asp Ala Glu Asn Leu Ile Tyr  
 260 265 270

Asp Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp Thr Met  
 275 280 285

Thr Val Asn Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr Asp Ser  
 290 295 300

Phe Ala Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile Ala Thr  
 305 310 315 320

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Gly Thr Tyr Asp Asn Thr Asn Lys Gln Ile Thr Tyr Thr Phe Thr Asp  
 325 330 335

Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu Thr Ser  
 340 345 350

Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu Asp Val  
 355 360 365

Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr Val Glu  
 370 375 380

Tyr Gln Lys Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser Met Phe  
 385 390 395 400

Thr Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile  
 405 410 415

Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly  
 420 425 430

Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys  
 435 440 445

Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile  
 450 455 460

Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln  
 465 470 475 480

Leu Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser  
 485 490 495

Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp  
 500 505 510

Tyr Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu  
 515 520 525

Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe  
 530 535 540

Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu Lys Thr  
 545 550 555 560

Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile  
 565 570 575

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Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr  
 580 585 590

Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser Val Arg Thr Asp Glu Glu  
 595 600 605

Gly Lys Tyr Gln Phe Asp Gly Leu Lys Asn Gly Leu Thr Tyr Lys Ile  
 610 615 620

Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro Thr Leu Lys His Ser Gly  
 625 630 635 640

Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn Ser Val Trp Val Thr Ile  
 645 650 655

Asn Gly Gln Asp Asp Met Thr Ile Asp Ser Gly Phe Tyr Gln Thr Pro  
 660 665 670

Lys Tyr Ser Leu Gly Asn Tyr Val Trp Tyr Asp Thr Asn Lys Asp Gly  
 675 680 685

Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser Gly Val Lys Val Thr Leu  
 690 695 700

Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Thr Thr Asp Glu Asn  
 705 710 715 720

Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser Gly Asn Tyr Ile Val His  
 725 730 735

Phe Asp Lys Pro Ser Gly Met Thr Gln Thr Thr Thr Asp Ser Gly Asp  
 740 745 750

Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu Val His Val Thr Ile Thr  
 755 760 765

Asp His Asp Asp Phe Ser Ile Asp Asn Gly Tyr Tyr Asp Asp Asp Ser  
 770 775 780

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
 785 790 795 800

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
 805 810 815



Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
			820					825					830		

Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His Asp Ser  
850 855 860

Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn Lys Asn  
885 890

<400> 53

Leu His Ile Gly Asn Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala  
20 25 30

Lys Arg Asn Leu Glu Asp Gly Glu Ser Ser Gln Phe Asp Asn Leu Lys  
50 55 60

Trp Leu Gly Leu Asp Trp Asp Glu Ser Val Asp Lys Asp Lys Gly Phe  
65 70 75 80

Gly Pro Tyr Arg Gln Ser Glu Arg Ala Glu Ile Tyr Asn Pro Leu Ile  
85 90 95

Gln Gln Leu Leu Glu Glu Asp Lys Ala Tyr Lys Cys Tyr Met Thr Glu  
100 105 110

Glu Glu Leu Glu Ala Glu Arg Glu Ala Gln Ile Ala Arg Gly Glu Met  
115 120 125

Pro Arg Tyr Gly Gly Gln His Ala His Leu Thr Glu Glu Gln Arg Gln  
130 135 140

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Gln Tyr Glu Ala Glu Gly Arg Lys Pro Ser Ile Arg Phe Arg Val Pro  
 145 150 155 160

Lys Asp Gln Thr Tyr Thr Phe Asn Asp Met Val Lys Gly Glu Ile Ser  
 165 170 175

Phe Glu Ser Asp Asn Ile Gly Asp Trp Val Ile Val Lys Lys Asp Gly  
 180 185 190

Val Pro Thr Tyr Asn Phe Ala Val Ala Val Asp Asp His Tyr Met Gln  
 195 200 205

Ile Ser Asp Val Ile Arg Gly Asp Asp His Val Ser Asn Thr Pro Lys  
 210 215 220

Gln Leu Met Ile Tyr Glu Ala Phe Gly Trp Glu Ala Pro Arg Phe Gly  
 225 230 235 240

His Met Ser Leu Ile Val Asn Glu Glu Arg Lys Lys Leu Ser Lys Arg  
 245 250 255

Asp Gly Gln Ile Leu Gln Phe Ile Glu Gln Tyr Arg Asp Leu Gly Tyr  
 260 265 270

Leu Pro Glu Ala Leu Phe Asn Phe Ile Thr Leu Leu Gly Trp Ser Pro  
 275 280 285

Glu Gly Glu Glu Glu Ile Phe Ser Lys Glu Glu Phe Ile Lys Ile Phe  
 290 295 300

Asp Glu Lys Arg Leu Ser Lys Ser Pro Ala Met Phe Asp Arg Gln Lys  
 305 310 315 320

Leu Ala Trp Val Asn Asn Gln Tyr Met Lys Thr Lys Asp Thr Glu Thr  
 325 330 335

Val Phe Glu Leu Ala Leu Pro His Leu Ile Lys Ala Asn Leu Ile Pro  
 340 345 350

Glu Asn Pro Ser Glu Lys Asp Arg Glu Trp Gly Arg Lys Leu Ile Ala  
 355 360 365

Leu Tyr Gln Lys Glu Met Ser Tyr Ala Gly Glu Ile Val Pro Leu Ser  
 370 375 380

Glu Met Phe Phe His Glu Met Pro Glu Leu Gly Lys Asp Glu Gln Glu

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385                      390                      395                      400

Val Leu Gln Gly Glu Gln Val Pro Glu Leu Met Asn His Leu Tyr Gly  
                                  405                      410                      415

Lys Leu Glu Ser Leu Glu Ser Phe Glu Ala Thr Glu Ile Lys Lys Met  
                                  420                      425                      430

Ile Lys Glu Val Gln Lys Glu Thr Gly Ile Lys Gly Lys Gln Leu Phe  
                                  435                      440                      445

Met Pro Ile Arg Val Ala Val Thr Gly Gln Met His Gly Pro Glu Leu  
                                  450                      455                      460

Pro Asn Thr Ile Glu Val Leu Gly Lys Asp Lys Val Leu Ser Arg Leu  
                                  465                      470                      475                      480

Lys Asn Leu Val

<210> 54

<211> 296

<212> PRT

<213> Staphylococcus epidermidis

<400> 54

Met Glu Tyr Lys Asp Ile Ala Thr Pro Ser Arg Thr Arg Ala Leu Leu  
  1                      5                      10                      15

Asp Gln Tyr Gly Phe Asn Phe Lys Lys Ser Leu Gly Gln Asn Phe Leu  
                                  20                      25                      30

Ile Asp Val Asn Ile Ile Asn Lys Ile Ile Glu Ala Ser His Ile Asp  
                                  35                      40                      45

Cys Thr Thr Gly Val Ile Glu Val Gly Pro Gly Met Gly Ser Leu Thr  
                                  50                      55                      60

Glu Gln Leu Ala Lys Asn Ala Lys Lys Val Met Ala Phe Glu Ile Asp  
  65                      70                      75                      80

Gln Arg Leu Ile Pro Val Leu Lys Asp Thr Leu Ser Pro Tyr Asp Asn  
                                  85                      90                      95

Val Thr Ile Ile Asn Glu Asp Ile Leu Lys Ala Asp Ile Ala Lys Ala  
                                  100                      105                      110

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Val Asp Thr His Leu Gln Asp Cys Asp Lys Ile Met Val Val Ala Asn  
 115 120 125

Leu Pro Tyr Tyr Ile Thr Thr Pro Ile Leu Leu Asn Leu Met Gln Gln  
 130 135 140

Asp Val Pro Ile Asp Gly Phe Val Val Met Met Gln Lys Glu Val Gly  
 145 150 155 160

Glu Arg Leu Asn Ala Gln Val Gly Thr Lys Ala Tyr Gly Ser Leu Ser  
 165 170 175

Ile Val Ala Gln Tyr Tyr Thr Glu Thr Ser Lys Val Leu Thr Val Pro  
 180 185 190

Lys Thr Val Phe Met Pro Pro Pro Asn Val Asp Ser Ile Val Val Lys  
 195 200 205

Leu Met Gln Arg Gln Glu Pro Leu Val Gln Val Asp Asp Glu Glu Gly  
 210 215 220

Phe Phe Lys Leu Ala Lys Ala Ala Phe Ala Gln Arg Arg Lys Thr Ile  
 225 230 235 240

Asn Asn Asn Tyr Gln Asn Phe Phe Lys Asp Gly Lys Lys Asn Lys Glu  
 245 250 255

Thr Ile Arg Gln Trp Leu Glu Ser Ala Gly Ile Asp Pro Lys Arg Arg  
 260 265 270

Gly Glu Thr Leu Thr Ile Gln Asp Phe Ala Thr Leu Tyr Glu Gln Lys  
 275 280 285

Lys Lys Phe Ser Glu Leu Thr Asn  
 290 295

<210> 55  
 <211> 106  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 55

Met Thr Ser Asn His His Ala Pro Tyr Asp Leu Gly Tyr Thr Arg Ala  
 1 5 10 15

Thr Met Asp Asn Thr Lys Gly Ser Glu Thr Ala Arg Ser Ser Lys Ser  
 20 25 30

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His Lys Val Val Leu Ser Ser Asp Cys Ser Leu Gln Leu Asp Tyr Met  
 35 40 45

Lys Leu Glu Ser Leu Val Ile Val Asp Gln His Ala Thr Val Asn Thr  
 50 55 60

Phe Pro Gly Leu Val His Thr Ala Arg His Thr Thr Arg Val Cys Asn  
 65 70 75 80

Thr Arg Ser Arg Trp Ser Asn His Leu Glu Leu Ala Val Glu Gly Gly  
 85 90 95

Thr Asn Asp Trp Gly Glu Val Val Thr Arg  
 100 105

<210> 56  
 <211> 442  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 56

Met Phe Phe Lys Gln Phe Tyr Asp Lys His Leu Ser Gln Ala Ser Tyr  
 1 5 10 15

Leu Ile Gly Cys Gln Lys Thr Gly Glu Ala Met Ile Ile Asp Pro Ile  
 20 25 30

Arg Asp Leu Ser Ser Tyr Ile Arg Val Ala Asp Glu Glu Gly Leu Thr  
 35 40 45

Ile Thr His Ala Ala Glu Thr His Ile His Ala Asp Phe Ala Ser Gly  
 50 55 60

Ile Arg Asp Val Ala Ile Lys Leu Asn Ala Ser Ile Tyr Val Ser Gly  
 65 70 75 80

Glu Ser Asp Asp Thr Leu Gly Tyr Lys Asn Met Pro Asn Gln Thr His  
 85 90 95

Phe Val Gln His Asn Asp Asp Ile Tyr Val Gly Asn Ile Lys Leu Lys  
 100 105 110

Val Leu His Thr Pro Gly His Thr Pro Glu Ser Ile Ser Phe Leu Leu  
 115 120 125

Thr Asp Glu Gly Ala Gly Ala Gln Val Pro Met Gly Leu Phe Ser Gly  
 130 135 140

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Asp Phe Ile Phe Val Gly Asp Ile Gly Arg Pro Asp Leu Leu Glu Lys  
 145 150 155 160

Ala Val Lys Val Glu Gly Ser Ser Glu Ile Gly Ala Lys Gln Met Phe  
 165 170 175

Lys Ser Ile Glu Ser Ile Lys Asp Leu Pro Asn Tyr Ile Gln Ile Trp  
 180 185 190

Pro Gly His Gly Ala Gly Ser Pro Cys Gly Lys Ser Leu Gly Ala Ile  
 195 200 205

Pro Thr Ser Thr Leu Gly Tyr Glu Lys Gln Thr Asn Trp Ala Phe Ser  
 210 215 220

Glu Asn Asn Glu Ala Thr Phe Ile Asp Lys Leu Ile Ser Asp Gln Pro  
 225 230 235 240

Ala Pro Pro His His Phe Ala Gln Met Lys Lys Ile Asn Gln Phe Gly  
 245 250 255

Met Asn Leu Tyr Gln Pro Tyr Thr Val Tyr Pro Ala Thr Asn Thr Asn  
 260 265 270

Arg Leu Thr Phe Asp Leu Arg Ser Lys Glu Ala Tyr His Gly Gly His  
 275 280 285

Ile Glu Gly Thr Ile Asn Ile Pro Tyr Asp Lys Asn Phe Ile Asn Gln  
 290 295 300

Ile Gly Trp Tyr Leu Asn Tyr Asp Gln Glu Ile Asn Leu Ile Gly Glu  
 305 310 315 320

Tyr His Leu Val Ser Lys Ala Thr His Thr Leu Gln Leu Ile Gly Tyr  
 325 330 335

Asp Asp Val Ala Gly Tyr Gln Leu Pro Gln Ser Lys Ile Gln Thr Arg  
 340 345 350

Ser Ile His Ser Glu Asp Ile Thr Gly Asn Glu Ser His Ile Leu Asp  
 355 360 365

Val Arg Asn Asp Asn Glu Trp Asn Asn Gly His Leu Ser Gln Ala Val  
 370 375 380

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His Val Pro His Gly Lys Leu Leu Glu Thr Asp Leu Pro Phe Asn Arg  
 385 390 395 400

Asn Asp Val Ile Tyr Val His Cys Gln Ser Gly Ile Arg Ser Ser Ile  
 405 410 415

Ala Ile Gly Ile Leu Glu His Lys Gly Tyr His Asn Ile Ile Asn Val  
 420 425 430

Asn Glu Gly Tyr Lys Asp Ile His Leu Ser  
 435 440

<210> 57  
 <211> 285  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 57

Leu Lys Lys Ile Leu Val Leu Ser Leu Thr Ala Phe Leu Val Leu Ala  
 1 5 10 15

Gly Cys Asn Ser Gly Asp Lys Thr Asp Thr Lys Asp Lys Lys Glu Glu  
 20 25 30

Thr Lys Gln Thr Ser Lys Ala Asn Lys Glu Asn Lys Glu Gln His His  
 35 40 45

Lys Gln Glu Asn Asp Asn Lys Ala Ser Thr Gln Leu Ser Glu Lys Glu  
 50 55 60

Arg Leu Ala Leu Ala Phe Tyr Ala Asp Gly Val Glu Lys Tyr Met Leu  
 65 70 75 80

Thr Lys Asn Glu Val Leu Thr Gly Val Tyr Asp Tyr Gln Lys Gly Asn  
 85 90 95

Glu Thr Glu Lys Lys Gln Met Glu Gln Leu Met Leu Glu Lys Ala Asp  
 100 105 110

Ser Met Lys Asn Ala Pro Lys Asp Met Lys Phe Tyr Gln Val Tyr Pro  
 115 120 125

Ser Lys Gly Gln Phe Ala Ser Ile Val Gly Val Asn Lys Asn Lys Ile  
 130 135 140

Phe Ile Gly Ser Thr Gln Gly Ala Leu Ile Asp Tyr Gln Thr Leu Leu  
 145 150 155 160

Asn Asn Gly Lys Glu Leu Asp Ile Ser Gln Leu Tyr Glu Asp Asn Lys  
165 170 175

Ser Gly Ala Ala Gln Lys Ala Asp Asp Pro Asp Lys Asn Ser Ala Asn  
195 200 205

Asp Gly Lys Leu Asp Asn Lys Thr Tyr Leu Trp Asp Asn Ile Arg Ile  
225 230 235 240

Ile Met Gly Thr Tyr Lys Ser Glu Lys Asn Lys Ile Ile Lys Leu Asp  
260 265 270

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<210> 58
<211> 498
<212> PRT
<213> Staphylococcus epidermidis
```

Met Ala Asn Lys Glu Ser Lys Asn Val Val Ile Ile Gly Ala Gly Val  
1 5 10 15

Asn Ile Lys Leu Tyr Glu Arg Leu Asp Arg Pro Gly Ile Glu Ser Ser  
35 40 45

Asn Tyr Thr Val Gln Gln Pro Asp Gly Ser Ile Asp Ile Glu Lys Ala  
65 70 75 80

Lys Glu Ile Asn Glu Gln Phe Glu Ile Ser Lys Gln Phe Trp Gly His  
85 90 95



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Leu Val Lys Ser Gly Asn Ile Ser Asn Pro Arg Asp Phe Ile Asn Pro  
 100 105 110

Leu Pro His Ile Ser Phe Val Arg Gly Lys Asn Asn Val Lys Phe Leu  
 115 120 125

Lys Asn Arg Tyr Glu Ala Met Arg Asn Phe Pro Met Phe Asp Asn Ile  
 130 135 140

Glu Tyr Thr Glu Asp Ile Glu Glu Met Arg Lys Trp Met Pro Leu Met  
 145 150 155 160

Met Thr Gly Arg Thr Gly Asn Glu Ile Met Ala Ala Ser Lys Ile Asp  
 165 170 175

Glu Gly Thr Asp Val Asn Tyr Gly Glu Leu Thr Arg Lys Met Ala Lys  
 180 185 190

Ser Ile Glu Lys His Pro Asn Ala Asp Val Gln Tyr Asn His Glu Val  
 195 200 205

Ile Asn Phe Asn Arg Arg Lys Asp Gly Ile Trp Glu Val Lys Val Lys  
 210 215 220

Asn Arg Asn Ser Gly Asp Val Glu Thr Val Leu Ala Asp Tyr Val Phe  
 225 230 235 240

Ile Gly Ala Gly Gly Gly Ala Ile Pro Leu Leu Gln Lys Thr Gly Ile  
 245 250 255

Pro Glu Ser Lys His Leu Gly Gly Phe Pro Ile Ser Gly Gln Phe Leu  
 260 265 270

Ile Cys Thr Asn Pro Asp Val Ile Asn Glu His Asp Val Lys Val Tyr  
 275 280 285

Gly Lys Glu Pro Pro Gly Thr Pro Pro Met Thr Val Pro His Leu Asp  
 290 295 300

Thr Arg Tyr Ile Asp Gly Glu Arg Thr Leu Leu Phe Gly Pro Phe Ala  
 305 310 315 320

Asn Ile Gly Pro Lys Phe Leu Arg Asn Gly Ser Asn Leu Asp Leu Phe  
 325 330 335

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Lys Ser Val Lys Pro Tyr Asn Ile Thr Thr Leu Leu Ala Ser Ala Val  
 340 345 350

Lys Asn Leu Pro Leu Ile Lys Tyr Ser Ile Asp Gln Val Leu Met Thr  
 355 360 365

Lys Glu Gly Cys Met Asn His Leu Arg Thr Phe Tyr Pro Glu Ala Arg  
 370 375 380

Asp Glu Asp Trp Gln Leu Tyr Thr Ala Gly Lys Arg Val Gln Val Ile  
 385 390 395 400

Lys Asp Thr Lys Glu His Gly Lys Gly Phe Ile Gln Phe Gly Thr Glu  
 405 410 415

Val Val Asn Ser Lys Asp His Ser Val Ile Ala Leu Leu Gly Glu Ser  
 420 425 430

Pro Gly Ala Ser Thr Ser Val Ser Val Ala Leu Glu Val Leu Glu Lys  
 435 440 445

Asn Phe Ala Glu Tyr Glu Lys Asp Trp Thr Pro Lys Leu Gln Lys Met  
 450 455 460

Ile Pro Ser Tyr Gly Lys Ser Leu Ile Asp Asp Val Lys Leu Met Arg  
 465 470 475 480

Ala Thr Arg Lys Gln Thr Ser Lys Asp Leu Glu Leu Asn Tyr Tyr Glu  
 485 490 495

Ser Lys

<210> 59  
 <211> 516  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 59

Met Lys Ile Phe Lys Thr Leu Ser Ser Ile Leu Val Thr Ser Val Leu  
 1 5 10 15

Ser Val Thr Val Ile Pro Ser Thr Phe Ala Ser Thr Glu Ser Thr Ala  
 20 25 30

Thr Asn Gln Thr Gln Gln Thr Val Leu Phe Asp Asn Ser His Ala Gln  
 35 40 45

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Thr Ala Gly Ala Ala Asp Trp Val Ile Asp Gly Ala Phe Ser Asp Tyr  
 50 55 60

Ala Asp Ser Met Arg Lys Gln Gly Tyr Gln Val Lys Glu Leu Glu Gly  
 65 70 75 80

Glu Ser Asn Ile Ser Asp Gln Ser Leu Gln Gln Ala His Val Leu Val  
 85 90 95

Ile Pro Glu Ala Asn Asn Pro Phe Lys Glu Asn Glu Gln Lys Ala Ile  
 100 105 110

Ile Asn Phe Val Lys Asn Gly Gly Ser Val Ile Phe Ile Ser Asp His  
 115 120 125

Tyr Asn Ala Asp Arg Asn Leu Asn Arg Ile Asp Ser Ser Glu Ser Met  
 130 135 140

Asn Gly Tyr Arg Arg Gly Ala Tyr Glu Asn Met Thr Lys Asp Met Asn  
 145 150 155 160

Asn Glu Glu Lys Asn Ser Asn Val Met His Asn Val Lys Ser Ser Asp  
 165 170 175

Trp Leu Ser Gln Asn Phe Gly Val Arg Phe Arg Tyr Asn Ala Leu Gly  
 180 185 190

Asp Ile Asn Thr Gln Asn Ile Val Ser Ser Lys Asp Ser Phe Gly Ile  
 195 200 205

Thr Lys Gly Val Gln Ser Val Ser Met His Ala Gly Ser Thr Leu Ala  
 210 215 220

Ile Thr Asp Pro Asn Lys Ala Lys Gly Ile Ile Tyr Met Pro Glu His  
 225 230 235 240

Leu Thr His Ser Gln Lys Trp Pro His Ala Val Asp Gln Gly Ile Tyr  
 245 250 255

Asn Gly Gly Gly Ile Asn Glu Gly Pro Tyr Val Ala Ile Ser Lys Ile  
 260 265 270

Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp Ser Ser Leu Val Glu Asp  
 275 280 285

Arg Ser Pro Lys Tyr Leu Arg Glu Asp Asn Gly Lys Pro Lys Lys Thr

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290

295

300

Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly Lys Leu Leu Asn Asn Leu  
 305 310 315 320

Thr Thr Trp Leu Gly Lys Lys Glu Ser Gln Ser Ser Met Lys Asp Met  
 325 330 335

Gly Ile Lys Leu Asp Asn Lys Thr Pro Leu Leu Asn Phe Glu Gln Pro  
 340 345 350

Glu Asn Ser Ile Glu Pro Gln Lys Glu Pro Trp Thr Asn Pro Ile Glu  
 355 360 365

Gly Tyr Lys Trp Tyr Asp Arg Ser Thr Phe Lys Thr Gly Ser Tyr Gly  
 370 375 380

Ser Asn Gln Arg Gly Ala Asp Asp Gly Val Asp Asp Lys Ser Ser Ser  
 385 390 395 400

His Gln Asn Gln Asn Ala Lys Val Glu Leu Thr Leu Pro Gln Asn Ile  
 405 410 415

Gln Pro His His Pro Phe Gln Phe Thr Ile Lys Leu Thr Gly Tyr Glu  
 420 425 430

Pro Asn Ser Thr Ile Ser Asp Val Arg Val Gly Leu Tyr Lys Asp Gly  
 435 440 445

Gly Lys Gln Ile Gly Ser Phe Ser Ser Asn Arg Asn Gln Phe Asn Thr  
 450 455 460

Leu Gly Tyr Ser Pro Gly Gln Ser Ile Lys Ala Asn Gly Ala Gly Glu  
 465 470 475 480

Ala Ser Phe Thr Leu Thr Ala Lys Val Thr Asp Glu Ile Lys Asp Ala  
 485 490 495

Asn Ile Arg Val Lys Gln Gly Lys Lys Ile Leu Leu Thr Gln Lys Met  
 500 505 510

Asn Glu Asn Phe  
 515

<210> 60  
 <211> 84  
 <212> PRT

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&lt;213&gt; Staphylococcus epidermidis

&lt;400&gt; 60

Gly Thr Pro Leu Glu Leu Val Phe Val Asn Thr Leu Gly Pro Lys Pro  
 1 5 10 15

Cys Phe Ala Lys Pro Asn Lys Ile Leu Leu Leu Glu Tyr Ile Pro Leu  
 20 25 30

Phe Val Ala Asp Ala Ala Ala Val Lys Thr Thr Lys Leu Thr Met Pro  
 35 40 45

Ala Ala Lys Gly Thr Pro Ile Ser Val Asn Asn Leu Thr Asn Gly Leu  
 50 55 60

Leu Ser Gly Ser Thr Leu Asn His Gly Met Thr Asp Met Ile Thr Ser  
 65 70 75 80

Lys Pro Pro Ile

&lt;210&gt; 61

&lt;211&gt; 54

&lt;212&gt; PRT

&lt;213&gt; Staphylococcus epidermidis

&lt;400&gt; 61

Ser Ser Leu Ser Thr Ile Ile Pro Phe Ser Leu Gly Ala Leu Gly Lys  
 1 5 10 15

Phe Asn Ser Phe Ile Glu Gln Ile Ile Pro Leu Glu Ser Thr Pro Arg  
 20 25 30

Asn Trp Ala Ser Leu Ile Thr Ile Pro Leu Gly Ile Thr Ala Pro Thr  
 35 40 45

Phe Ala Thr Thr Thr Phe  
 50

&lt;210&gt; 62

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Staphylococcus aureus

&lt;400&gt; 62

Met Lys Phe Lys Lys Tyr Ile Leu Thr Gly Thr Leu Ala Leu Leu Leu  
 1 5 10 15

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Ser Ser Thr Gly Ile Ala Thr Ile Glu Gly Asn Lys Ala Asp Ala Ser  
20 25 30

Ser Leu Asp Lys Tyr Leu Thr Glu Ser Gln Phe His Asp Lys Arg Ile  
35 40 45

Ala Glu Glu Leu Arg Thr Leu Leu Asn Lys Ser Asn Val Tyr Ala Leu  
50 55 60

Ala Ala Gly Ser Leu Asn Pro Tyr Tyr Lys Arg Thr Ile Met Met Asn  
65 70 75 80

Glu Tyr Arg Ala Lys Ala Ala Leu Lys Lys Asn Asp Phe Val Ser Met  
85 90 95

Ala Asp Ala Lys Val Ala Leu Glu Lys Ile Tyr Lys Glu Ile Asp Glu  
100 105 110

Ile Ile Asn Arg  
115